Scoring table:

201082 seqs,

Title: Perfect score:

US-09-004-395. 1719

protein -

080041 bacteriopha
Q45471 bacillus sp
Q57539 bacillus sp
Q85265 potato viru
Q47732 enterococcu
Q41374 spinacia ol
Q6123 potato viru
Q3760 streptococc
Q25968 plasmodium
Q41027 pisum sativ
Q3770 streptosate
Q45027 pisum sativ
Q30704 mycoplasma
Q9zkd7 helicobacte
Q40693 oryza sativ
Q51090 borrelia bu
Q53070 lactococcus
Q9zid9 actinobacil

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protein search, using sw model
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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P906691
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P906692
092HL3
092H23
092H23
092H20
092H2
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p96127 treponema p
083627 treponema p
083626 treponema p
092h13 haemophilus
092s55 arabidopsis
092s42 actinobacil
014789 homo sapien
006692 treponema p
051228 borrelia bu
092h10 haemophilus
083670 treponema p
04582 clostridium
051465 borrelia bu
057922 pyrococcus
092km9 helicobacte
029317 archaeoglob
060013 pneumocysti
024967 streptococc
022664 spinacia ol
06408 saccharomyc
027147 euplotes eu
057028 bacillus sp
051028 bacillus sp
051028 bacillus sp
051028 chizosacch
043044 schizosacch
076737 dictyostell
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Best Local Similarity 100.0%;
Matches 341; Conservative 0,
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P70856;
01-FEB-1997
01-FEB-1997
01-NOV-1998
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543210
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GE Y., CHARON N.;
"An unexpected flam homolog burgdorfer1.";
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EMBL; U62900; AAC44770.1; -.
SEQUENCE 341 AA; 38367 MW; 5
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STRAIN-212;
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AHETFKRYLKLREKISIAEGSFQNFYEKIESEKPEESSPKN
                                                                                                                           DLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMR
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Spirochaetaceae; Borrelia
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Pred. No. 7.8e-111;
; Mismatches 0;
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2: sp_bacteri:
3: sp_tungi:*
4: sp_human:*
5: sp_invern:*
5: sp_invern:*
6: sp_mammal:
7: sp_mhage:*
7: sp_phage:*
10: sp_plant:
11: sp_virus:
12: sp_virus:
13: sp_verteb:
14: sp_unclas:

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sp_bacteria:*
sp_fungi:* sp_human:*

sp_archea:*

sp_organelle:*
sp_phage:* sp_mammal: *

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A FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,

A LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN

ADOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,

A PETERSON J., KERLAVAGE A.R., OUACKENBUSH J., SALZBERG S., HANSON M.

A PETERSON J., KERLAVAGE A.R., OUACKENBUSH J., SALZBERG S., HANSON M.

AVAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,

AVAN VUGT R., PALMER N., MCDONALD L., ARTIACH P., BOWMAN C.,

A UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,

AS GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

AS GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

A GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

A GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

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A GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

A GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

AND MARKET M., ADMINISTRATION M., HANCH B.,

BURLAND M., AND M., MARKET M., ROBERTS K., HATCH B.,

BURLAND M., AND M., MARKET M., ROBERTS K., HATCH B.,

BURLAND M., AND M., MARKET M., ROBERTS K., HATCH B.,

BURLAND M., AND M., MARKET M., MARKET M., MARKET M., MARKET M.,

BURLAND M., MARKET M., MARK
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Best Local Similarity 98.8%;
Matches 337; Conservative
                                                        01-NOV-1996 (TIEMBLrel. 01, 01-NOV-1996 (TIEMBLrel. 01, 01-AUG-1998 (TIEMBLrel. 07, CHEA GENE (FRAGMENT).

Borrelia burgdorferi (Lyme d Bacteria; Spirochaetales; Sp
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Q44876;
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01-JUN-1998 (TIEMBLIEL. 06, Last sequence update)
01-WOV-1998 (TIEMBLIEL. 08, Last annotation update)
FLAGELLAR FILAMENT OUTER LAYER PROTEIN (FLAA).
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2; Mismatches 2;
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Matches 56
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Best Local S
Matches 66
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MEDLINE; 98438936.
OLD I.G., TRUEBA G.A., SAINT GIRONS
"A chea chew operon in Borrella burg
disease.";
Res. Microbiol. 148:191-200(1997).
EMBL; X91907; CAA63001.1; -.
NON_TER
1
SEQUENCE 66 AA; 7577 MW; D661371
          P96127;
P96127;
01-MAY-1997
01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. PORCELLA S.F., RADOLF J.D., NC SUBmitted (APR-1997) to the EMEMBL; U97363; AAB63367.1; SEQUENCE 243 AA; 27299 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bactería;
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01-JUL-1997 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
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l Similarity 100.0%;
66; Conservative
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56; Conservative
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Spirochaetales;
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             (TrEMBLrel.
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                                                                           PRELIMINARY;
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Pred. No. 0.05
33; Mismatches
             Created)
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Last
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EMBL/GenBank/DDBJ
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Pred. No. 4e-16;
0; Mismatches
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eri, the agent of Lyme
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
0UTER MEMBRANE PROTEIN, PUTATIVE.
SEQUENCE FROM N.A.

FRASER C.M., NORRIS S.J., WEINSTOCK G.M., I FRASER C.M., GMINN M., HICKEY E.K., CLAYTON SODERGREN E., HARDHAM J.M., MCLEOD M.P., S
                                                                                                                                                                                                                  FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G., DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A., SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J., SCHERGEN E., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T., MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S., HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 98332770.
FRASER C.M., NORRIS S.J., WE
DODSON R., GWINN M., HICKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 179:1230-1238(1997).
EMBL; U65743; AAB47846.1; -.
SEQUENCE 242 AA; 27234 MW: D6A
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MEDLINE; 97175551.

CHAMPION C.I., BLANCO D.R., EXNER M.M., ERDJUMENT-BROMAGE
"HANCOCK R.E., TEMPST P., MILLER J.N., LOVETT M.A.;
"Sequence analysis and recombinant expression of a 28-kilo
Treponema pallidum subsp. pallidum rare outer membrane pro
(Tromp2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treponema
Bacteria;
                                                                                                                                    Science
                                                                                                                                                         "Complete genome sequence spirochete.";
                                                                                                                                                                                                      HATCH B., HORST VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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                                                                                                                                      281:375-388(1998)
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Spirochaetales;
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Spirochaetales;
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L; Mismatches
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                     SALZBERG
                                          R., KETCHUM
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VENTER J.C.;

VENTER J.C.;

Submitted (MAR-1998) to the EN

SUBMI; AE001240; AAC65636.1; -

STOTENCE 242 AA; 27257 MW;
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WARD C.K., LUMBLEY S.R., LATIN "Haemophilus ducreyi secretes protein.";

J. Bacteriol. 180:6013-6022(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus ducrey...
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EMBL; AF057695; AAC79757.1; -.
SEQUENCE 4152 AA; 456173 MW; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma
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Pred. No. 67;
4; Mismatches
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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HINDERHOFER K., PRAENDL R.,
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"Seed-maturation-induced subset ot heat 
heat-shock-element-binding protein compl
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RTX PROTEIN.
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sapiens (Human).
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                                                                                                                                                                                                                                                                                     EKNNILLGSQKDNNLSGSAGDDLLIGGEG-NDTLKGSYGADTYIFSKGHGQD--IVYEDT 1147
                                                                                                                                                                                                                                                                                                          QSSAMIMPPFKIPFYSGESGNQFL--GKGLIDNIKTMKEIKVSVYSLGYEIDLEVLFEDM 189
                                                                                                                                                                                                                                                                                                                                                       VVDLGINNWSVLLTPSARLQAYVKNSVVA----PAVVKSESKRYAGDTILGVRVLFPSYS 131
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Best Local s
Matches 39
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Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JONES M.H., NUMATA M., SHIMANE M.;
"Identification and characterization of
related to the bromodomain genes RING3
Genomics 45:529-534(1997).
EMBL; AF019085; AAB87862.1; -
PFAM; PF00439; bromodomain; 2.
PROSTIE; PS00633; BROMODOMAIN_1; 2.
SEQUENCE 947 AA; 107891 MW; F6E3DC6
                                                                                                           SEQUENCE FROM N.A.

PORCELLA S.F., RADOLF J.D., NORGARD M.V.;

Submitted (APR-1997) to the EMBL/GenBank/DDBJ

EMBL; U97363; AAB63368.1; -.

SEQUENCE 234 AA; 26071 MW; 436529F1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
Eutheria; F
[1]
                                                                                                                                                                                                                              01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                       Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
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                                                                                                                                                                                                                      FLAA HOMOLOG-
                                                                                                                                                                                                                                                                                                                                                                           303
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                      KIPFYSGESGNQFLGKGLIDNIK-----TMKEIKVSVYSLGYEIDLEVLFEDMNGMEYA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAQALEKLEMQKISQMPQEEQVVGVKERIKKGTQQNIAVSSAKEKSSPSATEKVFKQQEI 177
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                                                                                                                                                                                                                                                                                                                                                                                                                   KSHSSKVKNFIFYVKDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLKAH-----
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  KVSFYR-RGYNSF
                                                                                                                                                                                                                                                                                                                                                                         ----ETFKRVLKLREKIS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRHCSEILKEMLAKKHFSYAWPFYNPVDVNALGLHNYYDVVKNPMDLGTIKEKMDNQEYK
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76; Conserv
                                                  39; Conservative
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                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                 Score 105.5; D
Pred. No. 3.3;
17; Mismatches
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Last sequence update)
Last annotation updat
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Pred. No. 19;
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F6E3DC61 CRC32;
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051228;
01-JUN-1998
01-JUN-1998
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MEDLINE: 9805943.

MEDLINE: 9805943.

MEDLINE: 9805943.

LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M., DOUGHERTY B., TOMB J.-F., FLEISCHANN R.D., RICHARDSON D., PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M., VAN YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTIERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; BB0210; -. PFAM; PF00515; TPR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:580-586(1997).
EMBL; AE001131; AAC66595.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
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Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SURFACE-LOCATED MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                        326
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  NELIENSKNKEAS
                                                     VEKIESEKPEESS
                                                                                                                                                                                                                             KSNSENILNDSOKIENDKONTNLSKEKNSENILKTPDNSKYSNNNNTTSLKKISSNSOKE
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                                                                                                              SELSPPSQTIIGKIYRPYSYLIKKELYEILDDINTGRVTLGKNRLKELIKKGLSNKFQKV
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                                                                                                                                                                       Similarity
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(TIEMBLrel. 06, Last sequence up
(TIEMBLrel. 10, Last annotation
ATED MEMBRANE PROTEIN 1 (LMP1).
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v: 128085 MW;
339
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Pred. No. 35;
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Q9ZHL0;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAY-1999
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LSPA2.
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  MEDLINE;
                                               Treponema
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            SEQUENCE
                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.";
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                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                      242
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BL; AF057696; AAC79761.1; -.
QUENCE 4919 AA; 542595 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NISNKIAVLHSLGNISLNSKDQVYNLGEIYAGNNISV------KAHQLKNDVKLMGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DITNYVDYVYSGASGIVKPEDMVVDLGI----NNWSVLLTPSARLQAY-VKNSVVAPAVV
                                                                                                                                                                                                 NKNMDHQPDK
                                                                                                                                                                                                                                                                                                                       KAFRVSKSHSSKVKNFIFYVKDLRVLYDKLSVSI------DSDIDSESVFKVY--
                                                                                                                                                                                                                                                                                                                                                                                                                       I - - DLEVLFE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                              GKIYAGRDLTFNKSNAGGKSEIINRGTI-NVKNKLSYDSDVSFENNMQSQKVDLYTKIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTKTKEGQASYKLYQASNGGHFGNDGSSG-----YSEGDLNIKGKFADLDNKLTVQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSESK - -
                                                                                                                                                                                                                       EKIESEKPEE
                                                                                                                                                                                                                                                FQNGEWAKNDTGTDSYDSTKASEKYKKVENVDHKENIDEHKLNIGKHEITVPGVSFENLN 1396
                                                                                                                                                                                                                                                                                               EDFKKDKGASKML------DLYPNTDKEKAKIFAGIIRNGNDTISDVESEDFKKKYSK 1336
                                                                                                                                                                                                                                                                                                                                              YYSGSSSNYINPVSYLAALGNANNSSNPHYLNTALKHILGNGWQDDLKKQENIKVLKQKW
                                                                                                                                                                                                                                                                                                                                                                                              AKSDI ELTFKTNGTHPVYLNFKSNNNEKKYRNSENTKNFKSIGDLINEALSDSAPEAIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KIPFYSGESG--NQFLGKGLIDNIK------TMKEIKVSVYSLGYE 179
                                                                                                                                                                                                                                                                        -----ETSGTESLRKLKAHETFKRVLKLREKISIAEG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 6.1%; l similarity 19.1%; 82; Conservative 5
  FROM N.A.
98332770.
                                   pallidum.
Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria;
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9 (TrEMBLrel. 10,
9 (TrEMBLrel. 10,
RNATANT PROTEIN 2.
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                                                                                                                                                                                                                        336
                                                                        08, Created)
08, Last sequence update)
08, Last annotation update)
R LAYER PROTEIN (FLAA-2).
                                                                                                                                                                                                                                                                                                                                                                      ----WSNPNYIPNISSRII----KDDVPNYP-LASSKMRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RYAGDTILGVRVLFPSYSQSSAMIMPPF----
                                                                                                                                                                                                                                                                                                                                                                                                                     ---DMNGMEYAYSMGTLKFKGWADLI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma
                                      Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 104.5; DB 2;
; Pred. No. 2.8e+02;
58; Mismatches 119;
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Last annotation update)
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                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision;
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Similarity

Conservative

59;

Mismatches

97;

Indels

77;

Gaps

12;

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RESULT
Q45882
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Best Local S
Matches 42
Query Match
Best Local S
Matches 54
                                                                                                                                                                 mosquitocidal protein with homologies delta-endotoxins.",
J. Bacteriol. 178:3099-3105(1996).
EMBL; X94146; CAA63860.1; -.
PPAN; PF00555; endotoxin; 1.
SEQUENCE 613 AA; 71172 MW; CF41527
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01-NOV-1996
01-NOV-1996
01-NOV-1998
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SEQUENCE FROM N.A.

PRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,

DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,

DODSON R., HANDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,

SODERGREN E., HANDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,

SODERGREN E., HANDHAM J.M., WITTERBACK T.,

KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,

KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,

KHALAK H., ARTIACH BOWMAN C., COTTON M.D., FUJII C., GARLAND

MCDONALD L., ARTIACH BOWMAN C., COTTON M.D., FUJII C., GARLAND

MCDONALD L., ARTIACH BOWMAN C., COTTON M.D., FUJII C., GARLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G., DODSON R., GWINN M., HICKEY E. K., CLAYTON W. KETCHUM K.A., SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J. KHALAK H., RICHARDSON D., HOWELL-J.K., CHIDAMBARAM M., UTTERBACK MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., BOWMAN C., COTTON M.D., FULL C., GARLAL MCDONALD L., GARLAL MCDONALD M.D., FULL C., GARLAL MCDONALD M.D., FULL C., GARLAL MCDONALD M.D., FULL C., GARLAL M.D., GARLAL M.D., FULL C., GARLA
                                                                                                                                                                                                                                                                                                                                                                             BARLOY F., DELECTUSE A., NICOLAS L., LECADET M. "Cloning and expression of the first anaerobic Clostridium bifermentans subsp. malaysia, enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium bifermentans. Bacteria; Firmicutes; Bac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HATCH B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VENTER J.C.
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5 (TrEMBLrel. 01,
3 (TrEMBLrel. 08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTS K., WATTHEY L., WEIDMAN J., SMITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROBERTS
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27.8%;
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                            5.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 102; DB Pred. No. 6; 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases.
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                                Score 101.5;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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annotation updat
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AE001168
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                                                                                                                                                                                                                                                                                                           Submitted (12-DEC-1997) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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8 AE000783
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                                                                                                                                                                                           /transl_table=11
translation="MRIDYIEPFLDAASSVLRDMLLVENIEMGKPGLKSINQKIKGVS"
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                                                                                                                                                protein (chex)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
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/db_xref="GI:2688603"
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FLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNITYFLKNLDK
ISNEMIFFPRE"
complement(6699..7745)
/genc="BB0674"
/note="hypothetical protein; identified by Glimmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="BB0673"
complement(6187..6702)
/gene="BB0673"
/note="similar to GP:140
identified by sequence s
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FNFVKVNSSLRKEFFYNFNTISNGYITFYINKLFEGKNSYTIYLIQKENKALYSSDII
KNYIKILLKYLVIKKCFEKGIELTTKNIESTSKAISNDTDFLDEKTAKLIISSFFK
YETLOTMSPISTUIALFSARARTPKYKNNPVKGFIGYDESWFSIKQSGSREYDSRIIK
ELSEIAKVNKM"
                                                                                                                                                                                                                                                                                  YYSPSEYRVIEMEKTKFYIDKYLQRKSDSILGIFLFTLFASFTIFLMNFYKFFKASFL
NPIILMTKILQDPLEYRKIQIFFTLSEEKVYELAKSFNNLLLKEKLNSKRKSKIPLEI
EXVKKIINKQEIK"
complement(7739. .8602)
/gene"BB0675"
complement(7739. .8602)
/gene="BB0675"
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/db_xref="plD:g3688610"
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TILNPIMLSLEKLRFLRULKFNDLIIEIYYNSKEKNLILIAFARTFSMSLLIPFTFFI
TILNPIMLSLEKLRFLRULKHSIINEKAYLKEKYPFILIKEKDDLIYSKSDEIFV
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 complement(8599.
/gene="BB0676"
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complement(6187. .6702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MIQKTTIAADSSSKPRGINYDTGIPFNVLIVDDSVFTVKQLTQI
FTSEGFNIIDTAADGEEAVIKYKNHYPNIDIVTLDITMPKMDGITCLSNIMEFDKNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIVGLAGSVEGSIIIDMDIETALFVAGKLNFEEYDDFDDEETKEMVAATLTEVONIIA
GNFVTTLHAKGFVFDITPPAFIYGENMKISNKGSEALIVPFSLPDGKIIEVNIAIRER
V"
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/transl_table=11
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/protein_id="AAC67021.1"
/db_xref="plu:92688604"
/db_xref="GI:2688604"
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identified by sequence similarity; putative"
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/note="similar to
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arity; putative"
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Best Local Similarity
Matches 1246; Conserv
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                                                                                                                                                    | caagtaamatgagatttaagggttttagagtttcaaaggtcacacagttcaaaagttaaaa
                                                                                                                                                                                                                                                                                                                                                                                  tagggtatgagatagatcttgaggttttatttgaagatatgaatggcatggaatatgctt 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caggtgatactattttgggggtaagagttttgtttccaagctattctcaatctgcta
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attctgatattgacagtgagtctgtatttaaagttttatgagacttagcggaactggaatccc
                                                                                                                                 CAAGTAAAATGAGATTTAAGGCTTTTAGAGTTCAAAGTCACACAGTTCAAAAGAGCAAA
                                                                                                                                                                                                                             atatteetaatatateateeagaattattaaagaegatgtteeaaattateetettgett 1178
                                                                                                                                                                                                                                                                                                       attctatgggtactttaaagtttaaagggtgggctgatttaatttggtcaaatcctaact 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAAGGTCTTATTGATAACATTAAAACCATGAAAGAAATTAAGGTATCTGTTTATAGTT
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                                                                                                                                                                                                                                                                                      ATTCTATGGGTACTTTAAAGTTTAAAGGGTGGGCTGATTTAATTTGGTCAAATCCTAACT
                                                                                                                                                                                                                                                                                                                                                                TAGGGTATGAGATAGATCTTGAGGTTTTATTTGAAGATATGAATGGCATGGAATATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttctttttgctcaagagactgatggattagcagagggttctaaaagggcagagcctggag
                                                        ATTTCATCTTTTATGTTAAAGATTTAAGAGTTCTTTATGATAAGTTGAGTGTTTCAATAG
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/gene="BB0676"
/gene="BB0676"
/note="smillar to GB:L42023 SP:P44755 PID:1004013
PID:1222502 PID:1204815 percent identity: 25.58;
identified by sequence similarity; putative"
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Pred. No. 2.7e-143;
D; Mismatches 9;
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300 698 638 180 578 120 518 60

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MEDLINE
REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atatt 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctatcgctgaaggctctttccaaaactttgtagaaaagattgagagtgaaaaaccttgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttcgtaaattaaaggcacacgaaacttttaaaagagttttaaagcttagagaaaaaattt 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCATCTCCGAAAAATTAGGTTTAAATTAATATGTAAAGCTACCTAAAAGGTTTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATGCCTGAAGGCTCTTTCCAAAACTTTGTAGAAAAGATTGAGAGTGAAAAACCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCGTAAATTAAAGGCACACGAAACTTTTAAAAGAGTTTTAAAAGCTTAGAGAAAAAATTT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCTGATATTGACAGTGAGTCTGTATTTAAAGTTTATGAGACTAGCGGAACTGAATCCC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia
AE001167
92688585
                                                                                                                                                                                                                 Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van Yugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst, Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.,T.F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujil,C., Cotton,M.D., Horst,J. Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C. Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                             Submitted (12-DEC-1997) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              burgdorferi group.

1 (bases 1 to 10016)
                                                                                                                                                                                                                                                                                                                                                                                                                           burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Spirochaetales; Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE001167.1
                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                           98065943
                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390 (6660), 580-586 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyme disease spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE001167
                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 10016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10016 bp DNA
burgdorferi (section
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84. .1217
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                                                                                                            /organism="Borrelia
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 SP:P54304 PID:1303805 GB:AL009126
                                                                                                          burgdorfer1*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the complete genome.
                                                                                                                                                                                                                                    Cotton, M.D., Horst, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Horst, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1598
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putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1204. .1890)
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2024..2785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYEITNFALKGHESRHNKLNWELKPHLGLGLYAVSLLFCNDKNNNVRALIRKTGSFVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MRVDLLPLVELSLYINLSFCCKDFSIFNRILEELKCHLILLGHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidase, putative"
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similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="phosphoglycerate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAC67009.1"
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by sequence
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ce similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:987641 percent
similarity; putati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:M14658 SP:P06616 PID:416295 PID:42767
PID:987641 percent identity: 37.85; identified by sequence
similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi
Bacteria; Spirochaetales;
burgdorferi group
Direct Submission
Submitted (03-OCT-1995) I.G.
Mycology, 28 rue du Dr Roux,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    1 (bases 1 to 332)
Trueba,G.A., Old,I.G.,
A cheA cheW operon in 1
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/proteoin_id="AAC67012.1"
/db_xref="pl0:g2688594"
/db_xref="g1:2688594"
/db
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97.6%;
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BBU28962 2700 bp
Borrelia burgdorferi i
U28962
91113814
U28962.1 GI:1113814
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/protein_id="CAA63002_1"
/db_xref="PID:g1019755"
/db_xref="GI:1019755"
/db_xref="SWISS-PROT:044737"
/translation="MEILDLENEELLGVFFEEAQN"
a 37 c 61 g 104 t
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258. .261
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/translation="DSDIDSESYFKVYETSGTESLRKLKAHETFKRVLKLREKISIAE
GSFQNFYEKIESEKPEESSPKN"
205. .256
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<1. .202
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/protein_id="CAA63001.1"
/db_xref="PID:g1019754"
/db_xref="GI:1019754"
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/organism="Borrelia burgdorferi"
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/clone_lib="Cos1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function="chemotactic response"
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                                     histidine
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Pred. No. 4.1e-31;
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                                  kinase (cheA) gene,
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            GAAGAGAATATT 184
                                                            TTGCTTT-----ACATATTAAAATAATAGGAAATAGTATATGGAAATATTAGATTTG
                                                                                                                                                                 CCTGAAGAATCATCTCCGAAAAATTAGGTTTAAATTAATATGTAAAGCTACCTAAAAGGT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2700) Trueba, G.A. and John Direct Submission
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1 (bases 1 to 2700)

Trueba,G.A., Old,I.G., Saint Girons,I. and a cheA cheW operon in Borrelia burgdorferi,
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Bacteria; Spirochaetales;
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Conservative
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                                                                                                                                                                                                                                                                         RVDYYLLIYSDIEGVKKSLDSSNLIESYLVDEFNVKEELKKLADEEIKDVDLDSNFVLN
DNFDFTEDEISDLLLEVENQKLFKVRLDFVKNDRMATISGLOWLQALKSIGKIFKSID
DSSELLADKEFDFVLYYLISNTSEESISKK KILPDVVSHFEIKNVNLESLKSVRLKED
DEAPFKENKNIKKNSPISVNLIRIDSKKIDYILNLVSEAVISKSSYNQINSEMITLFY
NENTYTDYQESFORNFLIDLKIVFKDAGLTLEDEIESHINSLMSFKMEKALKDISELR
NSFFRLLQNFKMTSGRLSRITTDLHESVLKTTMLFISNIFSRFKMEKALKDISELR
NSFFRLLDKSVIDDLYDPLMHCVRNSMHGLETVEERVKRGKSKAGTILRAKN
EGNVISIEIBDDGIGIDFKVLRKLIEKGTIKEDAITSDFELLNLIFAPGFFRAVOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MEILDLENEEILGVFFEEAQNLVDILEENIMSLEDDPNNSDTID
EIFRAAHTKASSASLDMMELSDFTH LYEDVFDAIRDGKVNINNDLVDLLLSSLDVIK
EMLALRIDGKYLKNISLDLKSKLKGFLVIDDGTFIKRFDGNSIKNNFCLESSDLEEIR
EGLGIGQKYLRISVVFNSNSNHEVENGGLKIFNILKNLGSVLHTIPKYEQIIEDKFLK
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95. .2689
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VIPLNNVLETHRITEHDIKLLENYHEVYNLRDEVISVLRLDKLFNITRODSLIEKFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="involved in chemc/product="histidine kinase"
/protein_id="AAB96835.1"
/db_xref="FID::91113815"
/db_xref="GI:1113815"
                                                                                                                                                                                                      VVNTSNMKIAIVVDSILGEEDFVVKPIKDKFSSSAGIVGATTLGNGKVVLIIDVFKLF
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/strain="CT-1"
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                     Score 164.4; DB 2
Pred. No. 8.8e-13;
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T.hyody:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-NOV-1991) J.G. Kusters, Inst. of Infectious Diseases and Immun., P.O.Box 80.165, 3508 TD Utrecht, THE NETHERLANDS
2 (bases 1 to 1260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachyspira hyodysenteriae
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Brachyspira hyodysenteriae.
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1 (bases 1 to 1260)
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hyodysenteriae flaA1 gene
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/strain="C5"
/db_xref="taxon:159"
27 32
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/product="flagellin
1004. .1030
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103. .1065
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Pred. No. 1e-05;
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Brachyspira hyodysenteriae
Bacteria; Spirochaetales; Spirochaeta
1 (bases 1 to 1140)
1 (bases 1 to 1140)
Koopman, M.B.H. and Kusters, J.G.
Treponema hyodysenteriae vaccine
Patent: EP 0534526-A 1 31-MAR-1993;
DUPHAR INTERNATIONAL RESEARCH B.V
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                       /note="putative" 50. .55
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27. .3
                                                                /db_xref="taxon:159"
/cell_line="CBS 513.
           /note-"putative"
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                                                                                                     /organism="Brachyspira hyodysenteriae"
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                                                                                                                                                                                                                                                                                                                                                                aattatgttgattatgtatattcgggcgcttctggtattgttaagccggaagatatggtt 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtagatcttgggataaataattggagcgttttacttactccttctgcaaggttgcaggct 760
                                                                          aaaaatttcatcttttatgttaaagatttaagagttctttatgataagctaagtgtttca 1294
                                                                                                                                                                                     gcttcaagtaaaatgagatttaaggcttttagagtttcaaagtcacacagttcaaaagtt 1234
                                                                                                                                                                                                                                 GAATACTTACCTAATGTTCGCGACAGAGTATTAGTAAGAGAACCTCT---TTATCCTAGA
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atagattctgatattgacagtgagtct 1321
                                               GGAGATTTCATCACCTTACGTTAAAGATGTAACACTTGAGTATGACGTAGTAGTTGTTGAT
                                                                                                                                           ATGATCCCTTCTGTTAAATTAGATTCTTTAGGTTTCTATAGAACTAAAGATACTAAAGGC
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Similarity 49.4%;
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/protein_id="CAAO1715.1"
/db_xref="pid:9904393"
/db_xref="gi:9904393"
/db_xref="sii:9904393"
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/translation="mkKLFVVLTSIFIAASAYGLTNSTLIDFALTGNADNLQAGEGDT
/translation="mkKLFVVLTSIFIAASAYGLTNSTLIDFALTGNADNLQAGEGDT
/translation="mkKLFVVLTSIFIAASAYGLTNTLEXBVLTSTLIDFALTGNADNLQAGEGDT"
vnLQNEFGELKSYPMCTYFNGWRQVRWENREYLLPNVRDRYLYERPLYPRWLPSVKLD
SLGFYRTKDTKGGDFITYVKDVTLEXBVVVVDFEEDIDDEATWQLLKTENDRKQAIES
ARIREQAELROLEGRRIGGTAADQGAAANTGAADTGAAQEQAQ"

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103. .159
103. .1065
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Pred. No. 1e-05;
0; Mismatches 369;
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                                                                                                                                           cttgttgaagggtgtatcttaaaggagcaaagttgataaattaaaattttactaataaaaa
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                                                                                                                                                                                                                                           Homo saplens AC006986
94753246
AC006986.2 G
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On May 5, 1999 this sequence version replaced g1:4337255.
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Direct Submission
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3 (bases 1 to 173956)
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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/db_xref="taxon:9606"
/clone="NH0155J05"
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Pred. No. 0.0005;
0; Mismatches 226;
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Australian jumper ant.
Mitochondrion Myrmecia pilosula
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Formicoidea; Formicidae; Myrmecia.
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nilarity 47.7%;
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Pred. No. 0.0019;
D; Mismatches 27
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tacatgaaaaggaaagctaaaagtattttatttttttatta
                                                                  gattattattcttgttgaagggtgtatcttaaaggagcaaagttgataaatttta
                                                                                                                                                                                                          tctttttgctatgtctttaataaaaacaatgcgctttaactatcctggtaagataaaaaa
                                                                                                                                                                                                                                                                          agaattttatgattcttttaataatggtgattataatgaatcttttgatgttaaggtcaa
                                                                                                                                                                                                                                                                                                                                              TTTTATTAAATTAAATAATTATTTATTAAACTTAAATTTATTTATTTATTTATTT
                                                                                                                                                                                                                                                                                                                                                                TATGATAAATTTTTTAATAATTAAAAATAATTTTACTTAAATATTTTATAAATTAAAAAT
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Crozier,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrial-DNA sequence evidence on the phylogeny jack-jumper ants of the Myrmecia pilosula complex Mol. Phylogenet. Evol. 4 (1), 20-30 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-OCT-1994) Ross
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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ozier,R.H.
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/note="intergenic space"
/130 c 63 g 520
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ILPFWILLIWTIMHLYFLHLTGSSNPLGINSULNKIPFNIYSTSDMLGFTISLLFFTL
LILMFPYLFSDADDNFLANNLVTPTHITQPEWYFLFAYSILRSIPNKLGGVIALFSSIC
ILYFLPMLTSKMNSSSFYPLSQFLIWLFFMTFMILTWLGSQVIEHPYIITAQFFSMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="cytochrome b"
/protein_id="AAA86971.1"
/db_xref="PID:g576757"
/db_xref="GI:576757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:13618"
/tissue_type="head and thorax
/dev_stage="adult worker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSNFILLKLSYKMWDYFIYDKFFNN'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84.8; DB 36;
Pred. No. 0.0096;
0; Mismatches 227;
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KEYWORDS
SOURCE
ORGANISM
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AL034559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on Apr 29, 1999 this sequence version replaced gi:4493963. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is not the entire insert of clone MAL3P7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
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On Apr
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1 (bases 1 to 253307)

011ver,K., Bowman,S., Harris,D., Lawson,D., Quail,M. and Barrell,B.
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AL034559.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         malaria parasite P. falciparum
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pr 29, 19
                                                                                                                                                                                                                                         NNNNNNSSSSSGKVDGINILNNSNINERLHTFSGVYSLNLNDEIKIEINKKDMEKN
DIHLISIDTISKIHARDLLKENKRKLENFQENIKHEHKDEVSLYVKKKKIKKKM"
                                                                                                                                                                                  AEGKSESHNKNNKDDIEDNDKDTIKDIHNNNNSSDNNDDEYQSANSPVESDIVKKEKK
KKIPINMETKKKRTMNGTKDPIHKTPYDINIVGILNKEDVSNKSNDYNTNKNIEKNNY
EKKGEYNPFHNNLTDMQNSILINIINNNVENSPHSPRMKKNVAKMLLKGNLNTANFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTNNI LNY NDHTLKLI CNITENNKA ILHSNKSNLQKNNI LMPSYMQKKGTHI RETIKN
VY NI NGEPSTSVENI TNGEHFI NGQYDALKNMSLNNY DHQHNNIMNNI SNKNKLFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB39023.1"
/db_xref="PID:e1407858"
/db_xref="PID:g4493964"
/db_xref="GI:4493964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinesin related protein, len: 1201 ma; Similarity to
kinesin related protein. D.melanogaster kinesin like
protein 67A (TR:P91945) BLAST Score: 664, sum P(2) =
1.9e-67; 28% identity in 707 ma overlap."
                                          /gene="MAL3P7.2"
join(5457. .5577
                                                                                                                                                        DDDT I KNMNSNK I SDKHNMKSNNI LNNENGK I NDKSKKCKN I NNNNNNNNNNNNNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="mrkTkNLNDPFFLNNYYYNKEENNPIIICSDEKERKTKIYSTNH/
/note="predicted using hexexon; MAL3P7.2 (PFC0865w),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="predicted using hexExon; MAL3P7.1 (PFC0860w),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cocation/Qualifiers
1. .253307
                     gene="MAL3P7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MAL3P7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone="MAL3P7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'chromosome=":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:5833"
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                                          .5577,5689. .5787,5923. .6077,6189. .6743)
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IKEFVMNRIFKRNCNDTNNYDNNSNNNNNNDNHNDNHSNNSGINSSFNNNNNVHNKNI
KNDLEISYCSONVILYENLTFYETIKIFLLYYKKNVDKYLNKRFTKIMDLDLVQYL
NDQIKNLMDEVKKKISIFICFLVKRDIYILDEPFIALDIKTKTKLKFFFDKIKKNNI
FICTHDIYEANNFANDIAVIKSGQIIFRGSKNSFQKLIEYKFTLNIQFNCLPNEEQTNI
YLSQEKIMSALNKKGVIKSPRKVANNYVDGYNVGRISSHESSINDKKKDNNDNNNDDD
NNKNNSVDHIDHLFDILVTNINEFTNNRDIIKKNIIKFIKGTRNENKNCFIFFNENHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein, len: /codon_start=1
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                                                                                                          YCTYKINELESLKKLLCYLNKFKNILTYQLKTIDIYYTYIYIYTLNEKKKLLKNIQDK
DIKYLIEIDPLFFLFFQNFKYFNELNNLLLMKNNHMQPISYNFAYLRDILVRGNENKN
IINSTNHDDNPYDINMYNNHNKYGKYKNNNNNNSFYNMRDDTELTDIEENISSKKKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGIQSYHNNNSINSNDDQKKKNNNNNNYYYYNNPDGLITNVKYKIRVGDYALLNSNEK
YFFNDININLKQNFINFNTVDDLSFNIYFNEWYYFSFFIVLEYQFNSFILNYNADILK
KNNLLTPRYDEINELNKEREITMEYKKTDEKEYQVNNEYINENVGYDEKGGKYKTELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN
SLELNDDILNIHENDKNSLLYNLHTNIINLKSSEFNINDLYKDVYTENEFENIKNLKI
NPHILKVVKNTEFYKNFIKDIKNLKNENHYTQYFNDDRKKLFFYNFVKNNLVETKYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKKEVINKS
SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVYKNMKRYI
TSIYIYIYIYYYMLFYSCVIYDDLVNTDELIETIENLGLDNEQLQKKKQMDDDEENYD
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/translation="MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIYIGNLD
/translation="MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYILAVDNFNGYKL
NRLTEGDIVIVFSQYGEPIDVNLVRDNETGKEGYCFLSYADQFSTILAVDNFNGYKL
LERPLVVDHILNYRLPKKYLKDADKNEYKPTGAEGGGYYNVVESEIKLSKYFDKI
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NFFTTY I KPTLLLKLKKDLGSSSFYWYKF I VPLFLLSFGLLI I KCVSLFGKVQN I DLD
YST I SSNHLKQST I NYF I LYKNEMNNNET LGYNKYNLNDDN I KKNLNNSYDK I LKKLE
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DDEDDDDDDSVDIKYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
                                                                        KFIEKEFSYNTYRNNKNNDENDEYGEYDNYDDNMIMSNTSNIMKKKNIKKQNIFKTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLLSVENVNYYKKQKNVKFSYLFGLSPQSEGFKGKGLYKNAPLYNKYENKQYGNPFHL
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/db_xref="PID:e1407903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYPYVTLESDKKINEKNERNEKNERNEKNERNEKNEKNGKNEKNKDILSSTNNNVVMK
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/db_xref="GI:4493965"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using hexExon; MAL3P7.4 (PFC0875w),
iypothetical protein, len: 3004 aa"
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11431. .20442
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/gene="MAL3P7.3"
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Query Match
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ttcttttaggaagcaatgaggggttttctttttgggtttt----tattaagtgattcaaga 179
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complement(23721. .24665)
/gene="MAL3P7.6"
/note="predicted using hexExon; MAL3P7.6 (PFC0885c),
/note="predicted using hexExon; MAL3P7.6 (PFC0885c),
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/gene="MAL3P7.5"
/note="predicted using hexExon; MAL3P7.5 (PFC0880c),
/note="predicted using hexExon; MAL3P7.5 (PFC0880c),
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YLYYFYYILCLEIVLYIEDYKEFLFMSFFCFLLLYGFNIFLSICJFSSLYLHSYILFL
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SFFNTSGDFVFLLINCIIYLSIVFYKLLQIIBSKETNOKNESSKTNYEEIILNNSYN
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VGVQRKKEDKKNRYFFFLKNFYLSNKEYKOPKENYEKNENFFFFIOKKHSENDLKRGNNY
DENNTIMGIYKVGEKVDSNNYISEDEININNGLMSGYLKNDIYMNELMDYNNHDFDD
UNTVDIEMGISEKSNIKEKMLYKETEIDKYYKGOSDDNDEEKHRKISGNYLIKNLNI
KMPYKIYTFSSIFNNDLNILYFFKYFFCNNKDNLKGSLOTIANGONYEINNKFINKK
NONEHISEKIQKNNERDYKIELFTMSIYEHFKIILTFKNIELINVEKIKKINNLHLIKN
VNLKCDHHINCNGLSGGMKKVELMINLLRDDXIIFLYKLNDDDDGCSGIYNILKILKN
NONEHISEKIGKNNERDYKIELFTMSIYEHFKIILTFKNIELINVEKIKINCHIKK
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NUKCCDHHINCNGLSGGMKKVELMINLLEDDKIIFLYKLNDDHIDFCSGIYTHIILKNI
NUKCCEPTRATETERVENINGHENDEN HENDEN HENDE
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RVYEODIQLYKGEGIYUNDENOFDDYIDKYSLYDLEKGKEDKOLRENMLKGRHOKNNY
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KFDESNDISYTSNDVLKGDDDMLSLFRRIYKESKRNKNKINKKKKKENELILLETYDIEK
TNMNQLGSNLSNSNYLECNISSNMNSVNEDIIHSFIKENILKIKFGIRNFVIYTHIYT
DILYYDYLYLFNKNKITYKNYTTNIKNNFKKFYSFQIKLKGIRDSKIIDYVHMFFSIN
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ETLETRNDTDVNKEVEININLFYNYTSIHSYAYYTNSLFNMLSDFQNILNKKSGNKNI
ILDGSTYDNIKVVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNIREECNANFRLSKN
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/gene="MAL3P7.6"
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/db_xref="GI:4493967"
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/gene="MAL3P7.5"
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K"
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YYIFKTMKKKKYNSKKKKGNLISLCKFHKILLNLMIDKYSYLHSYLSRNKYISIFHLF
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QEGLNGVYFENAKAGLWSSFAIREKTSFSSYNMTEEGYGNNSTYNMYSNKGYNNEMVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB39025.1"
/db_xref="PID:e1407860"
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Pred. No. 0.009
0; Mismatches
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (strain Dd2) blood stage DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The large diverse gene family var encodes proteins involved in cytoadherence and antigenic variation of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Su, X.Z., Heatwole, V.M., Wertheimer, S.P., Guinet, F., Herrfeldt, J.A., Peterson, D.S., Ravetch, J.A. and Wellems, T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variant-specific surface protein
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                  /translation="mvelakmgpkeaaaggddiedesakhmfdrigkdvydkvkeeake
rgkglqgrlseakfeknesdpqtpedpcdldhkyhtnvttnvinpcadrsdvrfsdey
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                                                                                                                /product="variant-specific
/protein_id="AAA75396.1"
                                                                                                                                                                                                             /gene="var-1"
join(7307. .1
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                                                                                                                                                                                                                                                                                                                               /note="putative"
/label=rif_homology
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2068. .2967
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                                                                                                                                                        /codon_start=1
                                                                                                                                                                          /note="blood
                                                                                                                                                                                           /gene="var-
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                                                                                                                                                                                                                                                                                                                                                                                                                            strain="Dd2"
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121 attttcttttaggaagcaatgaggggttttctttttgggtttttattaagtgattcaagat 180
                                                                                                                                                                                           61 atttaagatatttaagagatgaacaaaatttgaaagataatttagatcttttagtaaaag 120
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QACRAYQEYUENKKKEESGOTNNETULKANVQPODPEYKGYEYKEDVOP 10GNEYLLOK
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PTVTVDVCSIVKTLFKDTUNFSDACGLKYGKTAPSSWKCIPSDTKSGAGATTGRSGSD
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QTPDKWWNEHAESIWKGMICALTYTEKNPDTSARGDENKIEKDDEYYERFFGSTADKH
GTASTPTGTYKTOYDVEKYKLEDTSGARTPSASGTPLLSDTYLFPYFRYLEEWGON
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NNIDISHDGACMPPROXLCLYINHESOTENIKTOBUKKDAF KTAAAETFLSWOYY
KSKNDSEAKILDRGLIPSOTENSMATTFGDYRDICLATDISKKONDVARAKDKIGKF
SKDGSKSPSGLSRQEWWKTNGPEIWKGMLCALTKYVTDTDNKRKIKNDYSYDKVNOSQ
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ENLDVGSVTKNDKASH51LGDVGVLAAKTDAAEIIKRYKDQNIGUTDP1QOKDGDAKG
RAVRYSFADLGDIRGKDMWDEDKSSTDMETRLITYFKNIKEKHDGIKDMPKYTGDES
KKPAYKKLRADWWEANRHQVWRAMKCATKGIICPGMPVDDYIPQRLRWMTEWAEWYCK
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RYIYLEGDSGTDSGYTDHYSDITSSESEYEEMDINDIYVPGSPKYKTLIEVVLEPSGN
NTTASGNNTTASGNNTTASGKNTPSDTQNDIQNDGIPSSKITDNEWNQLKDEFISQYL
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FGNSGCSASANEONKNGEYKDAIDCMLKKLKDKIGECEKKHDOYSDTECSDTPOPOT
LEDETLDDDIETEEAKKNMERICIENYLKTAOOEDEGGCVPAENSEEPAATDGGKEF
EOTFYLKPEEEAVPEPPPPPOEKAPAPIPOPOPPTPTOLLDNPHYLTALYTSTLAW
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IDATDIENGVDSTVLEMRVSADSKSGFNGDGLENACRGAGIFEGIRKDEWKCRNVCGY
VVCKPENVNGEAKGKHIIQIRALVKRWVEYFFEDYNKIKHKISHRIKNGEISPCIKNC
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YNLLYLQAKTTSTNPGRTVLGDDDPDYQQMVDFLTPIHKASIAARVLVKRAAGSPTEI
AAAAPITPYSTAAGYIHQEIGYGGCQEQTQFCEKKHGATSTSTTKENKEYTFKQPPPE
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QKNIMDKLLNYEKDEADLCLEIHEDEEEEKEKGDGNECIEEGENFRYNPCSGESGNKR
YPVLANKVAYQMHHKAKTQLASRAGRSALRGDISLAQFKNGRNGSTLKGQICKINENY
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TCNRGERTKGYCRCNDDQVPTYFDYVPQYLRWFEEWAEDFCRKKNKKIKDVKRNCRGK
DKEDKDRYCSRNGYDCEKTKRAIGKLEYGKQCISCLYAGNPYUWINNOKEOFDKOKK
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WENETHSGDINSGIPSGNHVLNTDVSIQIDMDNPKTKNEITNMDTNPDKSTMDTILDD
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PINISDSTNSMDSLTSNNHSPYNDKNDLYSGIDLINDALSGNHIDIYDEMLKRKENEL
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Pred. No. 0.027; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC005139 256172 bp DNA HTG 01-APR-1999 Plasmodium falciparum chromosome 12, WORKING DRAFT SEQUENCE,
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1 (bases 1 to 2561/2)
Hyman,R.W., Fung,E.L., Oin,F., Tamaki,T., Kurdi,O.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                       n Apr 2, 1999 this sequence version replaced gi:4337170.
NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                     100700 a
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                                    /organism="Plasmodium
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                                                                                                                                    158845: contig of 32110 bp in length 159045: gap of unknown length 211538: contig of 52493 bp in length 211738: gap of unknown length 248106: contig of 36368 bp in length 248306: gap of unknown length 248306: gap of unknown length 256172: contig of 7866 bp in length.
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                                                                                                                                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 713)

Dechering, K.J., Kaan, A.M., Mbacham, W., Wirth, D.F., Eling, W., Konings, R.N.H. and Stunnenberg, H.G.

Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasit Plasmodium falciparum

Mol. Cell Biol. 19 (2), 967-978 (1999)
                                                                                                                                                              Toernooiveld 1, Nijmegen 652:
Location/Qualifiers
                                                                                                                                                                                 Submitted (12-NOV-1997) Molecular Toernooiveld 1, Nijmegen 6525 ED,
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AF034389
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Plasmodium falciparum
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    /gene="s16"
537. .710
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537. .>713
                                                                        /gene="s16"
                                                                                                         /strain="NF54"
/db_xref="taxon:5833"
                                                                                                                                     /organism="Plasmodium
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                                        Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, I Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L. Chromosome 2 sequence of the human malaria parasite Plasmodium
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(bases 1 to 14867)
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/protein_id="AAD12581.1"
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/db_xref="GI:3098291"
/translation="M"
a 50 c 20 g 31
               282 (5391), 1126-1132 (1998)
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/note="Pfs16"
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and Hoffman, S.L.

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                                 AATATATAAAATGTGTATAAATAAATAATTCTTTTTAATTTTATTTTTATAATTAAAT 7938
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4:282(5395):1827]]
                                                                                                                                                                                                                                            Similarity
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HEIYKLLEIENKYLNINSNIEPENKNLIOEMEFNLYYEREIKNEKNYIIKNIKKEIYKK
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NEYCTLIKKGKYDDDMTIYKLKEVIKATHHILCOKTKNLETEGSDIDYSTLINSLINK
FILNKLIIDKNEILFYECLLKILLNIKFVNFOSLCISLISLKNIYNILIRNNYIIVNNY
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FILNKLIIDKNEILFYECLLKILLNIKFVNFOSLCISLISLKNIYNINILIRNNYIIVNNY
LENDIKSESLYLCNIEF LOKLESIKLLSHYOK SINHHINLOTHNISCILKNILSVSN
RYIKHHEEDNEDOKOOYVCSLTELNILFERKIHHHYLIIDDLIKNYLNTYKSISID
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SSIFSKKRDSHKKGSSFRGREGEFINRKSGSFKYVJNRLLKKNYNNYGRNEHNGR
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TVYTKRLNNYKTYSAPVKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSYPRKRIKK
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/db_xref="GI:3845199"
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/gene="PFB0490c"
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/db_xref="PID:93845198"
/db_xref="GI:3845198"
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/db_xref="taxon:5833"
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Search completed: August 18, 1999, 17:16:47 Job time: 3453 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

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Run on: August 18, 1999, 16:24:08; Search time 148.09 Seconds (without alignments) 2809.571 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-004-395-1 1663 1 atgataatcttttttcaaaa.....atatccttgaagagaatatt 1663

Scoring table: IDENTITY_NUC

Searched: 311585 segs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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RESULT 2 x20248_02/c Continuation (3 of 10) of x20248 from base 200001 (Borrelia burgdorferi polynucleotide s WP Sequence split into 10 fragments LOCUS x20248 Accession x20248 WP Fragment Name Begin End	Oy 830 attitiggggtaagagtttigtitocaagctattcctcaatcatctgctatgattatgcca 889 1111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   11111   111111	Db 104963 GATTATGTATATTCGGGCGCTTCTGGTATTGTTAAGCCGGAAGATATGGTTGTAGATCTT 104904  Qy 710 gggataataattggagcgttttacttactccttcttctgcaaggtttgcaggcttaag 769
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Endoflagellum; sheath protein; bacteriacide; 43 kD; vaccine; Treponema hyodysenteriae.
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14-SEP-1992; 202796.
25-SEP-1991; EP-202478.
24-JUL-1992; EP-202273.
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PPSDB; R3379.

Vaccine to protect plys against swine dysentery - comprises Vaccine to protect plys against swine dysentery - comprises Treponema hyodysenteriae endo-flagellum sheath protein, applied orally or intranasally [Page 21-22; 34pp; English].

This sequence encodes the endoflagellum sheath protein of T. hyodysenteriae. The endoflagellum consists of at least four proteins, this protien forms the sheath of the flagellum and three proteins, of molecular weights 37, 34 and 32 kD, make up its core. Antibodies raised against the sheath protein have been shown to be bacteriacidal for T. hyodysenteriae. The 43 kD sheath protein can be used in the production of a vaccine against infections such as
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Pri binding proteins
Proceeding the Call State Composition of plasmodium. Var-7 belongs to Ct laim 4; Page 56-61; 96pp; English.

CC This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to CC the Duffy binding like (DBL) family of genes which have homology to the Duffy binding protein (DABP) and sialic acid binding protein (C (SABP) conserved regions (see T72889 and T72888 respectively). The var CC family of genes modulate cytoadherence and antigenic variation of CC plasmodium infected erythrocytes. SABP and the Duffy antigen binding CC protein (DABP) are soluble proteins that appear in the culture composition fiter infected erythrocytes release merozoites. DABP and SABP CC surface. These proteins are necessary for erythrocyte invasion by the compositions are for the treatment and prevention of the invention. CC The compositions are nucleotide sequence or encoded polypeptide of the CC compositions are used for the treatment and prevention of malaria, and CC compositions are used for the treatment and prevention of malaria. They care also used in the preparation of vaccines for inducing a protective immune response in a mammal to plasmodium merozoites (especially CC plasmodium falciparum or plasmodium merozoites (especially Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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12-SEP-1997 (first entry)
12-SEP-1997 (first entry)
Plasmodium var-7 gene.
DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
DBL binding like gene; Duffy antigen binding protein; erythrocyte;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
The management of the protein o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996; U09508.
07-JUN-1995; US-487826.
07-JUN-1995; US-487826.
USSH) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                     Query Match 4.0%;
Best Local Similarity 47.8%;
Matches 225; Conservative ·
                                                                                                                                                                                                                               for diagnosts, prevention and treatment of malaria.

Disclosure; p; English.

Sequence allows for production of antigenic malarial proteins, use diagnosis, prevention and treatment of the disease. The sequence mused in an expression vector, and signal and regulatory sequences used to stimulate production of other products.

Sequence 6124 BP; 2567 A; 602 C; 801 G; 2137 T; 17 Oth
                                                                                                                                                                                                                                                                                                                                                          WO9001549-A.
22-FEB-1990.
10-AUG-1989;
12-AUG-1988;
                                                                                                                                                                                                                                                                                         DNA encoding SERA antigen of Plasmodium falciparum also DNA encoding signal and regulatory sequences of diagnosis, prevention and treatment of malaria
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WPI; 90-083508/11.
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12-AUG-1988; US-231771.
(DART-) Dartmouth College.
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                                     /label-Allele . 3098. .31%
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/label=Allele
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3091. 3120
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/label=Complementary to
'~~ Alelle II, skips
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3082. .3151
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/label=Regulatory
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/note="Alelle I."
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Best Local Sin
Matches 219;
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28-SEP-1988: 103949.
12-MAR-1988: 103949.
18-MAR-1987: DE-708783.
04-DEC-1987: DE-741057.
(BEHW) Behringwerke AG.
Knapp B, Hundt E, Enders B
WPI: 88-272384/39.
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Plasmodium
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07-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                           The 140 kD antigen of Plasmodium falciparum merozoites encoded by thi sequence can be used in malaria vaccines, and antibodies raised against it are useful in passive immuno-prophylaxis. The antibodies, nucleic acids and proteins are also useful as diagnostic agents, and antibodies may be used for the recovery of high-purity proteins. Sequence 3975 BP; 1690 A; 393 C; 575 G; 1317 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
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Malaria-specific gene enco
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Disclosure; age 9; 18pp; german.
Proteins, transformed cells and antibodies, useful in r
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N81157
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Pred. No. 0.0037;
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                 18-MAR-1992.
08-SEP-1990; IP-117344.
08-SEP-1990; EP-117344.
(BEHW ) BEHRINGWERKE AG.
SCHOLT J, Knapp B, Hundt E
WPI; 92-089689/12.
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1596. .1720
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PstI digestion (construction of pompA-5)
amplified by PCR (the amplified fragment
for the construction of pompA-7)"
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2077. .3430
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/note= "1.3 kb DNA fragment
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To construct pompA-5, pUC18-SERP which carries the complete SERP gene on a 5.8 kb XbaI fragment (Knapp et al., Mol. Biochem. Parasitol. 32 (1989), 73-84) was digested with KpnI and PstI. A 1.3 kb DNA fragment (see features) was isolated and ligated into the respective sites of pSK vectors. Subcloning of the SERP fragment into pSK was performed in order to create the correct translational reading frame at the 3' end of the SERP coding region. The resulting plasmid pSK-SERP was digested with SmaI and KpnI, the 1.3 kb fragment was isolated and cloned into the respective sites of pHS164-L.

pompA-5 and pompA-7 both encode 451 amino acids of the SERP antigen.

sequence 3975 BP; 1690 A; 393 C; 575 G; 1317 T;
                   11-SEP-1985;
11-SEP-1984;
11-SEP-1984;
10-SEP-1985;
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N60472 standard;
N60472;
                                                                                                                 WO8601802-A.
27-MAR-1986.
                                                                                                                                                                                                                                                                                       Plasmodium
                                                                                                                                                                                                                                                                                                             Malaria vaccine;
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(HALL-)
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Best Local Similarity
Matches 212; Conser
23-OCT-1986: AU0092.
11-APR-1985; AU-001008.
11-APR-1985; AU-001008.
25-JUL-1985; AU-001640.
11-APR-1986; AU-056037.
(HALL-) HALL W & E INST MED.
(KEMP/) KEMP D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.

Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
                                                                                                                                27-JUN-1991 (first entry)
Sequence encoding the Asparagin
Ag319 of Plasmodium falciparum
Malaria vaccine; ss.
                                                                                                                                                                          N60392 standard; DNA; 1612
N60392;
                                                                                                                        Plasmodium
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86-094065/14.
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                                                                                                                                                 27-JAN-1992; 101271.
21-FEB-1991; DE-105348.
(BEHW ) BEHRINGWERKE AG.
Hundt E, Knapp B, Kupper
WPI; 92-286009/35.
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Q27886;
Q4-FEB-1993
                                                                                                                                                                                                                     EP-499834-A.
26-AUG-1992.
27-JAN-1992;
21-FEB-1991;
DNA coding protein GBP 130 h and proteins produced - used vaccines to control malaria Claim 1; Page 12-14; 17pp; German.
Glycophorin binding protein 130h is a P.falciparum blood santigen 69% homologous with the known GBP130. The GBP130h its homologues can be used in vaccines to protect against caused by P.falciparum. The coding sequence was isolated u
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Plasmodium falciparum; mala
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Matches
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26-AUG-1986; US-900401.
(SLOK) SLOAN KETTERING:
Pologe L, Ravetch JV;
WPI; 92-199590/24.
                                                                                                                                                                                                                                                                                                                                                                                                                           US5116965-A.
25-MAY-1992.
26-AUG-1986;
26-AUG-1986;
                    Histidine-rich protein associated with Plasmodium knob phenotype and DNA encoding it, used for in vitro diagnosis of P. Falciparum infection.

Claim 1; Fig 4A-D; 29pp; English.

Two variants of HisRP are produced by P. falciparum. One is associated with what is referred to as "knobby phenotype" (K30) and "knobless phenotype" (K-). The "knobby" and "knobless phenotypes have been implicated in cytoadherence, which is characteristic of a part through the product of the company of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     techniques on a genomic P.falciparum FCBR strain library. GBP130h gene was found to be highly conserved between diff strains but is distinct from the GBP130 gene. See Q27878-Q27885 and Q33432.

Sequence 2418 BP; 1047 A; 303 C; 292 G; 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoding the Histidine-rich protein (HisRP) the knob (K+) phenotype.
Malaria vaccine; Histidine-rich protein; cytoadheren
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2909. .2911
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A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMP1) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMP1 polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the pfEMP1 protein of the MC type of Plasmodium falciparum. An alternative with the PfEMP2 polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1996; U05798.
27-APR-1995; US-430908.
(AFFY-) AFFYMAX TECHNOLOGIES NV.
BARUCH DI, HOWARD RJ, PASIOSKE
WPI: 96-497376/49.
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96-497376/49.
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10-AUG-1989; 003422.

12-AUG-1988; US-231771.

(DART-) Dartmouth College.

Inselburg JW, Bzik DJ;

WPI; 90-083508/11.
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Disclosure; p; English.

Disclosure; p; English.

Sequence allows for production of antigenic malarial proteins, useful diagnosis, prevention and treatment of the disease. The sequence may bused in an expression vector, and signal and regulatory sequences may lused to stimulate production of other products.

Sequence 6124 BP; 2567 A; 602 C; 801 G; 2137 T; 17 Others;
                          15-SEP-1996 (first entry)
Human 3' apolipoprotein B SAR element clone Rh32.
Erythropoietin; EPO; anaemia; gene therapy; vector;
scaffold attachment region; SAR element; apolipoprotein
transgenic animal; ss.
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Claim 8; Page 59-60; 84pp; Eng
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27-JUN-1996.
18-DEC-1995; CA0696.
19-DEC-1994; US-358918.
(CANG-) CANGENE CORP.
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D 09-JUN-1994.

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P 02-DEC-1993; AU0617.

R 03-DEC-1992; AU-006206.

R 16-DEC-1992; AU-006380.

N (UNIX) UNISEARCH LTD.

I Flores MV, Osullivan WJ, Stewart TS;

R WPI; 94-200271/24.

R WPI; 94-200271/24.

R P-PSDB; R55694.

R Nucleic acid encoding carbamoyl phosphate synthetase II -
1 isolated from Plasmodium falciparum, used to develop prods. for
T the treatment of malaria.

The treatment of malaria.

S Disclosure; Page 6-16; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.4%;
Best Local Similarity 44.4%;
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The CDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSI) of Plasmodium falciparum was determined. The CDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSB and CPSD.
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aaacgaaaattttataaaagatttatatataaggagttggtttacatgaaaaggaaaagct 487
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/EC_number= 6.3.5.5
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58: em_est26:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES 8

Result

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RESULT C83838/c LOCUS

DEFINITION

ACCESSION NID VERSION

C83838 3707 bp mRNA EST 28-APR-1999 C83838 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA cione SSA355, mRNA sequence. C83838 g2706770 C83838 1 G1:2706770

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The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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Dictyostelium discoideum.

Dictyostelium discoideum

Eukaryota; Dictyosteliida;

1 (bases 1 to 3707)
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, i
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA
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Institute of Biological Sc
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AU006427 Bombyx mori p50(Daizo) Bombyx mori cDNA clone wv41020.
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T = 'CREST project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7091"
/clone="wv41020"
/clone_lib="Bombyx mori p50(Daizo)"
/close_lib="59 g 322 t
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/strain="p50(Daizo)"
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Best Local Similarity 47.8%;
Matches 215; Conservative
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                                                       AATTAATTIGAAATGAAATGTTATTCGTTTTTAAATATATCTAGTTTTTATAGAAAAAA 316
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1 (bases 1 to 717)
Mita, K., Morinyo, M., Shimada, T., Okano, K. and Maeda, S. Establishment of cDNA database of Bombyx mori Unpublished (1999)
On Oct 6, 1998 this sequence version replaced gi:3709815.
                                                                                                                                                                                                                                                                                                                         Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nifs.go.jp
PROJECT = 'CREST project by JST'.
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                                                                                                                                                                                                       /clone_lib="Bombyx mori p50(Daizo)" 21 c 59 g 333 t
                                                                                                                                                                                                                                    /organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="e40883"
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                                                                                                                Score 62.4; DB 45;
Pred. No. 0.17;
0; Mismatches 231;
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                                                                                                                                                                                                                                                                                                       University of Washington
Department of Molecular Biotechnology, Box 357730, University of
Washington, Seattle, WA 98195
Tel: 5105280100
Fax: 5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate Cancer Expression Profiling by cDNA Sequencing Analysis Unpublished (1999)
On May 18, 1998 this sequence version replaced qi:3137424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
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AI525944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang, G.M., Ng, W., Farkas, J., Chen, L.,
                                                        h 3.7%;
Similarity 41.3%;
87; Conservative
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                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="pu-145"
/note="organ: Cell line; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a prostate tumor cell line DU-145."
a 62 c 77 g 145 t 106 others
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                                                        Score 61.4; DB 47; Pred. No. 0.24; 0; Mismatches 265;
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                                                                                                                                                                                                                Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
PROJECT = 'CREST project by JST'.
                                                                                                                                                                                                                                                                                                     Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S. Establishment of cDNA database of Bombyx mori Unpublished (1999)
On Oct 8, 1998 this sequence version replaced gi:37262
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AU001063 Bombyx mori
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1 (bases 1 to 688)
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/db_xref="taxon:7091"
/map="8"
                                                                                                      /clone_lib="Bombyx mori p50(Daizo)"
33 c 55 g 315 t
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/strain="p50/Daizo)"
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                                  Score 60.8; DE Pred. No. 0.3; 0; Mismatches
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University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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AA949610 EST 25-NOV-1998
LD29568.5prime LD Drosophila melanogaster embryo poT2 Drosophila
melanogaster cDNA clone LD29568 5prime similar to U37541:
Drosophila melanogaster complete mitochondrial genome, mRNA
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 593)

Warney D. Hong I. Evang-Holm M. Bondloton I. Su G.
                                                                                                                                                                             Email: http://www.fruitfly.org/EST, plate: 295 row: F column: 8
High quality sequence stop: 494.
Location/Qualifiers
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                                 /clone="LD29568"
/clone=llb="LD Drosophila melanogaster embryo po"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
   /note="Organ: embryo; Vector:
xhoI; Sized fractionated cDNA;
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pOT2; Site_1: EcoRI; Si
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                                                                Eukaryota; Dictyostellida; Dictyostellum.

1 (bases 1 to 578)

Yoshino,R., Morio,T. and Tanaka,Y.

Developmental cDNA in Dictyostellum discoideum
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced
                                                                                                                                                                                                 C90014 578 bp mrNA
C90014 Dictyostelium discoideum SS
discoideum cDNA clone SSG892, mrNA
          Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki
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C90014.1 GI:3059634
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ilarity 45.5%;
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d402hu@sakura.cc.tsukuba.ac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGAATTTTTTTTTTAATACGACGGGAATTGATTAGATTTTGTGCGTTTTAATTTGGAT 334
                                                     Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uex84.nirs.go.jp
PROJECT = 'CREST project by JST'.
                                                                                                                                                                       Mita, K., Morimyo, M., Shimada, T., Establishment of cDNA database of Unpublished (199)
On Oct 8, 1998 this sequence vers
                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombyx.
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AU001091 Bombyx mori
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/clone="$SG892"
/clone="11b="Dictyostelium d
/clone_11b="Dictyostelium d
/dev_stage="slug"
a 40 c 91 g 209 t
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1. .578
/organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium
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/db_xref="taxon:44689"
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p50(Daizo) Bombyx
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Pred. No. 0.58;
0; Mismatches 178;
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RESULT
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Best Local S
Matches 194
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                                                                Department of Molecular Biology University of Central Florida Orlando, FL 32816-2360 Tel: 407 384 2061 Fax: 407 384 3095
                                                                                                                                                                                                                   Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the plasmodium falciparum genome project Mol. Bjochem. Parasitol. 79, 1-12 (1996)
                                                                                                                                                                                                                                                                                                                                       malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N98113 315 bp mRNA EST 2203C3 czapPFDd2.1, Debopam Chakrabarti Plasmodium cione PF2203C, mRNA sequence.
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                                                                                                                                                   Contact: Debopam Chakrabarti
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Similarity 48.3%;
94; Conservative
                                 il: dchak@pegasus.cc.ucf.edu
primer: T3.
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/Clone="fbm0036f"
/Clone_1ib="Bombyx mori p50(Daizo)"
a 22 c 59 g 343 t 1 (22 c 59 g 343 t )
Location/Qualifiers
1. .315
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Pred. No. 0.
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                                                G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                         BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version
                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 564)

Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokytein,P., Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA536356 564 bp mRNA
LD16932.5prime LD Drosophila
              Email: http://www.fruitfly.org/EST, Plate: 169 row: C column: 8
                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                               AA536356.1 GI:2794386
EST.
                                                                                                                           Contact: Harvey, D.
                                                                                                                                                                                                                                                                                                                                            fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila
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Similarity 51.6%;
32; Conservative
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quality sequence stop: 421
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/lab_host="E. coli XL-1 blue"
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Pred. No. 0.97;
0; Mismatches 124;
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                                   est@fruitfly.berkeley.edu
                                                                                                                                                              replaced
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Length 338; Indels

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0

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150

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210

SS

(H.Urushihara)"

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AUTHORS
TITLE
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C90212.1
                                                   Yoshino,R., Morio,T. and Tanaka,Y. Developmental cDNA in Dictyostelium Unpublished (1997)
On Jan 19, 1998 this sequence versio
                                                                                                                                        Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostelium.
1 (bases 1 to 338)
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deum cDNA clone SSI382, mR
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26 c 53 g 298 t 1 others
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/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
         Hideko
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/organism="Drosophila melanogaster"
/organism="BDGP_EST:BDCln016123"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1292425 645 bp mRNA EST 01-DEC-1998 GHL5320.5prime GH Drosophila melanogaster head pOT2 brosophila melanogaster to M37275: https://doi.org/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10
                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 645)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brokstein, P., Levis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:800275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes. CI
AI292425
                                                                                       Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305
Email: d402hu@sakura.cc.tsukuba.ac.jp.
Email: http://www.fruitfly.org/EST, Plate: 153 row: B column: 8 High quality sequence stop: 613.

Location/Qualifiers
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/strain="AX4"
/strain="taxon:44689"
/clone="SSI382"
/clone_lib="Dictyostelium d
/dev_stage="slug"
a 21 c 7 g 133 t
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AI296407
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 671)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                         Drosophila
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH15320"
/clone_lib="GH Drosophila melanogaste
/sex="male and female"
/dev_stage="adult"
/dev_stage="adult"
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/note-"Organ: head; Vector: pOI
xhoI; Sized fractionated cDNAs
pOT2. plasmid cDNA library."
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G. M. Rul
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University of California Berkeley
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Site_2: Xhol; Sized fractionated cDNAs were directly
ligated in pOT2. Plasmid cDNA library.
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/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
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/db_xref="taxon:7227"
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                              tatgtctttaataaaaacaatgcgctttaactatcctggtaagataaaaaagattattat 358
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g4418136
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BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: 271 row: C column: 6 High quality sequence stop: 655.
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/note="Organ; head; Vector: pOT
/note; Sized fractionated cDNAs
xhol; Sized fractionated cDNAs
pOT2. Plasmid cDNA library."
43 c 72 g 383 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="GH Drosophila melanogaster head
/sex="male and female"
/dev_stage="adult"
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/db_xref="taxon:7227"
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  239
                                                                                                                                                      122 ttttcttttaggaagcaatgaggggttttctttttgggttttt---attaagtgattcaag
                                                                                                                                                                                                              152 AGAATAATTTTTTGACATTTAGAGTATGTGAAGGGGCCTTAGGTTTATCAATTTTAGTT
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 708)

E Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,

S Harvey, D., Hong, L., Evans-Holm, G.M.

Brokstein, P., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (1997)

On Mar 20, 1998 this sequence version replaced gi:297999
                                                                                                                                                                                                                                    tttaagatatttaagagatgaacaaaatttgaaagataatttagatcttttagtaaaaga 121
                                                                                                                                                                                                                                                                                            TTAATATTATTTTTATATTATTTATTTATTTAAATATATTAAATTATGAAAGTTATTTT 151
tgattcttttaataatggtgattataatgaatcttttgatgttaaggtcaatctttttgc
                                         atttttatattcttttttaaagaatggagtttattatgtaaatctttcaagagaatttta
                                                                                                                         TCTATAATTCGTACTCATGGTAATGATTATTTTCAATCTTTTAGAATTATATAATGTTAA 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of California Berkeley 539 LSA, Berkeley, CA 94720-3200, Fax: 510 643 9947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.
Plate: 276 row: C column: 1
High quality sequence stop: 647.
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/gex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
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Pred. No. 0.86;
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Search completed: August 18, 1999, 17:04:38 Job time: 2784 sec

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Alpha-amylase vari Variant alpha amyl

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd
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OM protein - protein search, using sw model

9 August 18, 1999, 17:20:03 ; Search time 13:23 Seconds (without alignments) 610.504 Million cell updates/sec

Title: Perfect score: Sequence: US-09-004-395-2 1719 1 MKRKAKSILFFLLS' MKRKAKSILFFLLSTVLFAQ......FQNFVEKIESEKPEESSPKN 341

Scoring table: BLOSUM62 188963 seqs, 23686106 residues

Searched:

Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A_Geneseq_36:*

#### SUMMARIES

Result No.

esult NO: 1	Score 324.5 125.5 110 110 109	18.9 7.3 6.4	Length 320 242 1657 1805 444 947		ID R33279 W22133 W81355 W73896 R34719 R34719 R34719	cription cription be endoflage ponema palli pleuropneumc pleuropneumc pluropneumc pluropneumc pluropneumc
10 10	10 8.		947 450 419 713		0711 9876 0103 6010	W09904265 Seq ID N H. pylor1 GHPO 109 Mycoplasma 46-48 k Canine zona pelluc
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43	87	5.1	714	<b>~</b> +	E6000A	Enterococcus faeca

Query Match 18.9%; Score 324.5; DB 1; Best Local Similarity 28.4%; Pred. No. 2.9e-24; Matches 89; Conservative 63; Mismatches 130;

Indels 31; Gaps

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Length 320;

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::||: :: 277 --ARIREQAELRD 287 307 RVLKLREKISIAE 319 164 QNEFGELKSYPMGTVYFNGWRQVRWENREYLPNVRDSVLVRE-PLYPRMIPSVKLDSLGF 222

EDMNGMEYAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMFFKAFRV 246

187

PT orally or intranasally PS Claim 2; Page 21-22; 34pp; English. CC This sequence represents the endoflar CC hyodysenteriae. The endoflagellum or CC proteins, this protien forms the sheat CC proteins, of molecular weights 37, 3 CC Antibodies raised against the sheath CC bacteriacidal for T. hyodysenteriae. CC be used in the production of a vacci CC swine dysentery. SQ Sequence 320 AA;		RESULT 1  R33279  ID R33279 standard; Protein; 320 AA.  AC R33279;  DT 16-JUL-1993 (first entry)  DE 43 kD endoflagellum sheath protein.  KW bacteriacide: 43 kD; vaccine; infection:
Claim 2; Page 21-22; 34pp; English. This sequence represents the endoflagellum sheath protein of T. This sequence represents the endoflagellum consists of at least four proteins, this protien forms the sheath of the flagellum and three proteins, of molecular weights 37, 34 and 32 kD, make up its core. Antibodies raised against the sheath protein have been shown to be bacteriacidal for T. hyodysenteriae. The 43 kD sheath protein can be used in the production of a vaccine against infections such as swine dysentery.  Sequence 320 AA;	Treponema hyodysenteriae.  Key  Location/Qualifiers  peptide  /note= "Signal peptide"  20320  protein  20320  Indra 1993  13-MAR-1993  14-SEP-1991; EP-202478  24-JUL-1992; EP-202478  (DUIN ) DUPHAR INT RES BV.  (ROUDHAR LINT RES BV.  KRODDHAN MBH, Kusters JG;  WPI; 93-102665/13.  N-PSDB; Q38583  Vaccine to protect pigs against swine dysentery - comprises  Treponema hyodysenteriae endo-flagellum sheath protein, applied	ALIGNMENTS  T 1  33279 standard; Protein; 320 AA.  R33279;  16-UUL-1993 (first entry)  43 kD endoflagellum sheath protein.  Badoflagellum; sheath protein; 1, hyodysenteriae; core; antibody;  badteriacide; 43 kD; vaccine; infection; swine dysentery.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Treponema pallidum outer membrane protein - used in detection and induction of immune response in an animal to pathogenic Spirochaetales Claim 1; Fig 11; 77pp; English.

This rare outer membrane protein (OMP) of species Treponema pallishers rare outer membrane protein (OMP) of species (TROMP2 gene) subspecies pallidum is encoded by a 765 bp sequence (TROMP2 gene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SLOK ) SLOAN KETTERING INST CANCER RES.
(REGC ) UNIV CALIFORNIA.
Blanco Dr. Lovitt MA, Miller JN, Temp:
WPI: 97-393614/36.
N-PSDB: T76579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in ice cold sodium citrate buffer, incubated with occasional vortexing to release the outer membrane from the inner membrane Treponemal protoplasmic cylinders were removed by centrifugation. The outer membrane in the supernatant was subjected to SDS-PAGE to obtain the rare OMP. The recombinant expression of the rare OMP can be used for diagnostic tests to detect syphilis and for development of host immunity during syphilis.
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23-JAN-1996;
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                                                                                                       YIPNISSRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKVKNFIFYVKDLRVLYDKLSVSI
                                                                                                                                                                      GKGLIDNIKTMKEIKVSVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPN
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NMHID
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Ilidum rare outer membrane protein (TROMP-2).
membrane protein; Treponema pallidum; Spirochaetales;
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/note=
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                                                                                                                                           FDVWVWGAGYQYSLEALVRDCTGRVHTLLIGNLDFQGWKNLSVSVPT
                                                                     RYLGSAQHLSFVGFRIRTSPSERVDDFY-----VFFDQFKALA
                                                                                                                                                                                                                                                                                                                                                             7.3%; Score 125.5; DB 1; 22.4%; Pred. No. 0.00012; Live 31; Mismatches 104;
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This sequence represents the ApXIV toxin serotype 1 isolated from Actinobacillus pleuropneumoniae strain 4074 (serotype 1 reference strain). The invention relates to an attenuated live Actinobacillus pleuropneumoniae microorganism producing no functional ApXIV toxin. The invention also provides a subunit vaccine for protecting an animal envention also provides a subunit vaccine for protecting an animal apainst infection of A. pleuropneumoniae, the vaccine contains pure ApXIV toxin and a pharmacologically allowable carrier. The pure ApXIV toxin and a pharmacologically allowable carrier of an antibody against apXIV for distinguishing A. pleuropneumoniae infection from A. suis.

N.B. This sequence was indexed from EP-875574, which is the first major country equivalent to JP10290695.
16-APR-1999 (first entry)
A. pleuropneumoniae ApxIV toxin serotype 1 protein sequence
                                                              W73896 standard;
W73896;
                                                                                                                                                                                                                                                                                                                                                                                        1039
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Frey J, Segers RPAM
WPI; 99-027956/03.
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10-APR-1997;
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A. pleuropneumoniae ApxIV toxin serotype 1 protein sequence.

ApxIV toxin; ATX toxin; attenuated microorganism; subunit vaccine;

A pleuropneumoniae infection; diagnosis.
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                                                                                                                                                                                                                                                                                                                      KRVLKLREKISIAEGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSSAMIMPPFKIPFYSGESGNQFL--GKGLIDNIKTMKEIKVSVYSLGYEIDLEVLFEDM 189
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                                                                                                                                                                                                                                                                                                                                                                                    DSVTVKSFYSHVD---YQFDKLEFA-DRSITRDELIKAGLHLYGTDGNDD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSKVKNFIFYVKDLRVLYDKLSVSIDSDIDSESVFK----VYETSGTESLRKLKAHETF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGMEYAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMRFKAFRVSKS
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                                                                                                   Protein; 1805
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Pred. No. 0.081;
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RESULT
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                             03-OCT-1992;
09-OCT-1991;
02-SEP-1992;
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N.B. This sequence was indexed from EP-875574, which is the first major
                                                                                                           Bacillus subtilis srfA operon Mulienzyme complex; surfactin Bacillus subtilis. Ep-540074-A. 05-MAY-1993.
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This sequence represents the ApxIV toxin serotype 1 isolated Actinobacillus pleuropneumoniae strain 4074 (serotype 1 reference).
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A pleuropneum
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                                                                                                                                                                                                                                                                                                            R34719 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSILEGGKGNDILRGGY 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRVLKLREKISIAEGSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NW------AATSNLTIARLREAGVIFAESTDLKGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSKVKNFIFYVKDLRVLYDKLSVSIDSDIDSESVFK----VYETSGTESLRKLKAHETF 305
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  ENIRICERCHE SPA
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                          203037.
IT-MI2683.
IT-MI2044.
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                                                                                                                                                                                                                                                                                                            Protein; 444
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Pred. No. 0.
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Rodriguez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Bacillus subtilis chromosomal DNA region comprises the srfA operon which encodes the multienzyme complex surfactin synthetase (MCSS). Analysis of the sequence showed four regions potentially coding for proteins, a zone upstream of the first ORF contg. the srfA operon promoter and a presumed terminator positioned downstream of the stop codon of the fourth ORF. Chromosomal DNA downstream of the ORF4 stop codon was also sequenced, sharing four regions (ORF5-8) potentially coding for different prods. ORF6 and ORF7 are contiguous and are potentially transcribed in the opposite direction to srfA from a single promoter situated between ORF7 and ORF8. ORF8 is
N-PSDB; V68343.

Transcriptional regulator gene containing bromodomain sequence be expressed in testis tissue and is useful in treatment of car
                                                                                                                           29-OCT-1990; J01782.
17-APR-1998; J01782.
18-APR-1997; JP-116402.
                                                                                                                                                                                                                                    Homo sapiens. wo9848015-A1.
                                                                                                                                                                                                                                                                                Transcriptional regulatory factor RING3. Human; transcriptional regulatory factor; testis specific bromodomain; testicular ce
                                                                                                                                                                                                                                                                                                                                                               W81168 standard;
W81168;
05-MAR-1999 (fin
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Claim 15; Page 50-51; 70pp; English
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                                                                               28-JAN-1999.
15-JUL-1998; U14679.
22-JUN-1998; US-102322.
17-JUL-1997; US-09164.
10-OCT-1997; US-061599.
10-OCT-1997; US-061765.
10-OCT-1997; US-061765.
11-OCT-1997; GB-021697.
[LUDW-] LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and other proliferative disorders
Claim 1; Page 19-24; 42pp; Japanese.
Claim 1; Page 19-24; 42pp; Japanese.
The present sequence represents the human transcriptional regulatory factor RING3, which is isolated from testicular cells. RING3 contains a testis specific bromodomain (TSB) which is expressed specifically in testis tissue and also expressed in certain tumour lines. The transgenic cells may be used to express RING3 which is a TSB expression protein. The TSB expression product can be used in the treatment of cancer and other proliferative disorders, and in screening of compounds for ability to bind to it (e.g. for use as drugs by modulation of transcriptional regulation). DNA capable of hybridising to RING3 polynucleotides may be used for construction of probes and primers.
                                                                 Chen Y,
                                                                                                                                                                                                                                                                                   Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                    Tureci
                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                     prostate cancer.
                                                                                                                                                                                                                                                                                                                     WO9904265 Seq ID No:
                                                                                                                                                                                                                                                                                                                                                                    07114 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSEDERVKRLAKLQEQLKAVHQQLQVLSQVPFRKLNKKKEKSKKEKKKEK 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AYSMGTLKFKGWADLIWSN-----PNYIPNISSRIIKDDVPNYPLASSKMRFKAFRVS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRHCSEILKEMLAKKHFSYAWPFYNPVDVNALGLHNYYDVVKNPMDLGTIKEKMDNQEYK
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                                  Ö
                                                                    Gout
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M, Sahin U,
 cancer
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associated nucleic acids and polypeptides
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                                                 Scanlan
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Pred. No. 0.067;
0; Mismatches 120;
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MJ, Stockert
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Best Local
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                                                                                        08-OCT-1998.

01-APR-1998; U06371.

29-JUL-1997; US-902615.

01-APR-1997; US-833457.

24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers Disclosure; Page 728-730; 787pp; English.

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions
                                                                                                                                                                                  peptic ulcer disease
Helicobacter pylori.
W09843478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                   (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
                                                                                                                                                                                                                                          H. pylori GHPO 1097 protein. GHPO protein; Helicobacter i
                                                                                                                                                                                                                                                                                 31-MAR-1999
                                                                                                                                                                                                                                                                                                    W98762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAQALEKLFMQKLSQMPQEEQVVGVKERIKKGTQQNIAVSSAKEKSSPSATEKVFKQQEI
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                                                                                                                                                                                                                           ulcer disease.
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76; Conservative
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PO 1097 protei
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18.5%;
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                                                                                                                                                                                                                                            infection; gastroduodenal disease; gastritis;
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Best Local S
Matches 63
                                                                                                                                                                                                                                                    19-SEP-1996; AU0149.
15-MAR-1996; AU-001789.
16-MAR-1995; AU-001789.
(UYME) UNIV MELBOURNE.
Doughty SW, Lee R, Wall
WPI; 96-433763/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 8; Page 1640-1642; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                   Putative protective antigens against Mycoplasma detection, prevention or treatment of Mycoplasma hyopneumoniae in swine Disclosure: Fig 7: 43pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma 46-48 kDa protective antigen. Antigen; vaccine; mycoplasmal pneumonia;
Ayopheumwater and the projective antigen Disclosure; Fig 7; 43pp; English.

The gene (T38241) coding for a 48 kDa putative protective antigen The gene (T38241) coding for a 48 kDa putative protective antigen The gene (T38241) coding for a 48 kDa putative protective antigen (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd. from a Mycoplasma hyopneumoniae genomic librar (W01037) was obtd.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a stop codon"
101
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is a stop codon"
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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T13814-16). The antigen had originally been isolated from M. hyponeumoniae cells using antibody probes enriched with Mycopl specific antibodies. Other protective antigens were also iden (see also W01024-31). Protective antigens and antibodies can used in vaccines for preventing or treating mycoplasmal infect partic. M. hypneumoniae infections in swine. They can also b for diagnosis.
New DNA sequence encoding canine zona pellucida CZP2 - useful for the prodn. of a canine contraceptive vaccine antigen claim 1; Page 8-10; 10pp; Japanese.

The CZP2 DNA (Q70072) was prepd. by the cloning of CZP2(75-520) - Q81700 using the primers given in Q70073-74, CZP2(1-65) - Q81804 using the primers given in Q70082-83, CZP2(42-103) - Q81803 using the primers given in Q70079-81 and CZP2(487-713) - Q81957 using the primers given in Q70075-78.
                                                                                                                            N-PSDB; Q70072.
                                                                                                                                                                                                                                          antigen
                                                                                                                                                                                                                                                        Canine;
                                                                                                                                                                                                                                                                    Canine zona
                                                                                                                                                                                                                                                                                  R60101;
15-MAR-1995
                                                                                                                                                                                                                                                                                                              R60101 standard; Protein;
                                                                                                                                                                      25-DEC-1992; 359265.
25-DEC-1992; JP-359265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ELMKNSQNKIIDLSPEGENAVYVPGWNYGTAGQRIQSFLTINKDPAGGNKIKAVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGK--GLIDNIKTMKEI------KVSVYSLGYEIDLEVLFEDMNGMEYAY--SMGTLK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NGSGVGTAVNTIADKGIPIVAYDR---LITGSDKYDWYVSFDNEKVGELQGLSLAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQ-------F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RWISAQKDIISYVDETEAATSTITKNQD-----AQNNW---LTQQANLSPAPKGFIIAPE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---STRLDLTNYVDYVYSGASGIVKPEDMVVDLGINNWSVLLTPSARLQAYVKNSVVAPA 106
                                                                                                                                                                                                                             familiaris.
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                                                                                                                                                                                                                                                       dog;
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pellucida CZP2
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Query Match Best Local Matches 7

19; Conser

Conservative

73;

Score 97.5; I Pred. No. 0.38 73; Mismatches

97.5; No. 0

DB .38;

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Length

Indels

127;

Gaps

22

5.7%; 19.4%;

Match

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                                 HGE-25. This polypeptide is useful in the treatment of Ehrlichia infection, and as a vaccine for the prevention of infection. Such vaccines comprise an immunogenic portion of an Ehrlichia antigen associated with human granulocytic ehrlichiosis (or a variant) and is thus especially useful in the treatment of human granulocytic ehrlichiosis (HGE). The polypeptides, antigenic epitopes or DNA molecules can be combined with a suitable carrier in pharmaceutical compositions. Such compositions and vaccines are useful to manufacture medicaments for inducing protective immunity against Ehrlichia infection in patients especially against HGE. HGE is caused by a rodent bacterium normally transmitted to humans by the same tick which transmits Lyme disease and babesiosis. Co-infection with these diseases is thus possible and the compositions of the invention may be used in methods to detect at least one of Ehrlichia infection, Lyme disease or B. microti infection in
                                                                                                                                                                                                                                                                                            Example 1; Page 125-127; 140pp; English. This sequence represents an immunogenic HGE-25. This polypeptide is useful in thinfection, and as a vaccine for the previous
                                                                                                                                                                                                                                                                                                                                                                                                       Poly:peptide(s) comprising immunogenic portion of Ehrlichia antigen and encoding DNA sequences, useful for e.g. diagnosis and treatment of Ehrlichia infection, especially human granulocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1998; U05695.
20-NOV-1997; US-975762.
21-MAR-1997; US-821324.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia sp. extended HGE-25 protein.

Ehrlichia sp. extended HGE-25 protein.

Antigen; human granulocytic entichiosis; HGE; diagnosis; treatme immunogenic; infection; vaccine; epitope; medicament; rodent; bac protective immunity; Lyme disease; babesiosis; detection; HGE-25.
                                                                                                                                                                                                                                                                                                                                                                                     ehrlichiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; V69430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia sp. WO9842740-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W82656 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TMKEIKVSVYSL---GYEIDLEVLFED-----MNGMEYAYSMGTLKFKGWADLIWSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                           portion of Ehrlichia antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment;
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74

DMVV-----DLGINNWSVLLTPSARLQAYVKN----

Query Match Best Local S Matches 68

Similarity

5.78;

Score Pred.

97.5; No. 0.

DB .28;

1.

Length Indels

Mismatches

101;

75;

Gaps

16

-SVVAPAVVKSE

68;

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia sp.
WO9842740-A2.
01-OCT-1998.
23-MAR-1998; U05695.
                               associated with human granulocytic ehrlichiosis (or a variant) and is thus especially useful in the treatment of human granulocytic ehrlichiosis (HGE). The polypeptides, antigenic epitopes or DNA molecules can be combined with a suitable carrier in pharmaceutical compositions. Such compositions and vaccines are useful to manufacture medicaments for inducing protective immunity against Ehrlichia infection in patients especially against HGE. HGE is caused by a rodent bacterium normally transmitted to humans by the same tick which transmits Lyme disease and babesiosis. Co-infection with these diseases is thus possible and the compositions of the invention may be used in methods to detect at least one of Ehrlichia infection, Lyme disease or B. microti infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIMAR-1999 (first entry)
Ehrlichia sp. extended HGE-15 reverse complement protein.
Antigen; human granulocytic ehrlichiosis; HGE; diagnosis; treatment; immunogenic; infection; vaccine; epitope; medicament; rodent; bacter protective immunity; Lyme disease; babesiosis; detection; HGE-15.
Ehrlichia sp.
patients.
Sequence
                                                                                                                                                                                                                               This sequence represents an immunogenic portion of Ehrlichia anti
HGE-15. This polypeptide is useful in the treatment of Ehrlichia
infection, and as a vaccine for the prevention of infection. Such
vaccines comprise an immunogenic portion of an Ehrlichia antigen
                                                                                                                                                                                                                                                                                                        Example 1; Page 111-113; 140pp; English.
                                                                                                                                                                                                                                                                                                                                         Poly:peptide(s) comprising immunogenic portion of Ehrlichia antigen - and encoding DNA sequences, useful for e.g. diagnosis and treatment of Ehrlichia infection, especially human granulocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1997; US-975762.
21-MAR-1997; US-821324.
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                                                                                                                                                                                                                                                                                                                                                                                                                  98-609891/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEIKVSVYSL-GYEI---DLEVLFEDMNGMEYAYSMGTLKFKG-----WADLIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMVVEKFAHDLGIR-----VGSNSLRSLIKNIRIFQDANGVFDQERYEAVLADSGMTES 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNPNYIPNISSRIIKD--DVPNYPLA---SSKMRFKAFRVSKSHSSKVKNFIFYVKDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEISSDAVDISGSDISDDELQKLFEE----QYKNSLNFPEYRSADYIIMAEDDLLADVIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RVLYDKLSVSIDSDIDSESVFKVYE----TSGTESLRKLKAHETFKRVL-KLREKIS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDQEVDVEIKNSELHDQRDVLNLVFTDKNEAELAYKAYQEGKSFEELVSDAGYTIEDIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Å
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                                                                                                                                                                                                                                                                                         portion of Ehrlichia antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .24;
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                                   possible detect at ection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
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231 NNISKDYLPYGYRNYVFALNEGEVSEMFRSYVGWHIMKVIRKHEITKEDLEKLKEKIS

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                           New isolated granulcytic erhlichia nucleic acids - used to develop products for use in vaccines for inhibiting Ehrlichiosis and for use in detection and diagnosis claim la; Fig 1; 184pp; English.

This sequence represents the granulocytic ehrlichia (GE) protein W20. which has been isolated from HL60 cells infected with Ehrlichia sp. G is an acute potentially fatal tick borne infection and the proteins is an acute potentially fatal tick borne infection and exercised in this invention can be used in vaccines to elicit a beneficial immune response in an animal to GE. They can be used for inhibiting Ehrlichoisis in an animal. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia sp. Wzv.1 pr...
Granulocytic ehrlichia; GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AQUI-) AQUILA BIOPHARMACEUTICALS INC. Beltz 6, Coughlin RT, Murphy C, Storey WPI, 99-034663/03.
N-PSDB; V65139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1998; U08264.
25-APR-1997; US-044869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-1999
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                                                                                                                                                                                                                                                               74 DMVV-----DLGINNWSVLLTPSARLQAYVKN------SVVAPAVVKSE
                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                              S-----KRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKGLIDNIKTM 166
                                                                                                                                                                                                                              DMVVEKFAHDLGIR-----VGSNSLRSLIKNIRIFQDANGVFDQERYEAVLADSGMTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RVLYDKLSVSIDSDIDSESVFKVYE----TSGTESLRKLKAHETFKRVL-KLREKIS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNPNYIPNISSRIIKD--DVPNYPLA---SSKMRFKAFRVSKSHSSKVKNFIFYVKDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEISSDAVDISGSDISDDELQKLFEE----QYKNSLNFPEYRSADYIIMAEDDLLADVIV 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYVNKIRNALPSTIL-MECLEPNRAE-----LHIPYYDALAKDVVLGL-LQHRVADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RVLYDKLSVSIDSDIDSESVFKVYE----TSGTESLRKLKAHETFKRVL-KLREKIS 316
                                SDQEVDVEIKNSELHDQRDVLNLVFTDKNEAELAYKAYQEGKSFEELVSDAGYTIEDIAL
                                                               SNPNYIPNISSRIIKD--DVPNYPLA---SSKMRFKAFRVSKSHSSKVKNFIFYVKDL--
                                                                                               VEISSDAVDISGSDISDDELQKLFEE-----QYKNSLNFPEYRSADYIIMAEDDLLADVIV 170
                                                                                                                                                             SYVNKIRNALPSTIL-MECLFPNRAE-----LHIPYYDALAKDVVLGL-LQHRVADI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDQEVDVEIKNSELHDQRDVLNLVFTDKNEAELAYKAYQEGKSFEELVSDAGYTIEDIAL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                             and diagnosis.
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o. W20.1 protei
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                               5.7%;
22.8%;
                                                                                                                                                                                                                                                                                               54;
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diagnosis; Ehrlichoisis.
                                                                                                                                                                                                                                                                                                               Score 97.5; DB Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                               101;
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                                                            DNA and peptide of mycoplasma hyopneumoniae - useful for diagnosts and treatment of swine mycoplasmal pneumonia plasmats and treatment of swine mycoplasmal pneumonia plasmats and primers used in a method of diagnosing mycoplasmal pneumonia of swine.

Wycoplasmal cells were collected from the culture of M.hp, lysed in a mycoplasmal pneumonia of swine.

Wycoplasmal cells were collected from the culture of M.hp, lysed in a culfer containing SDS, followed by the extraction of DNA and cells containing SDS, followed by the extraction of DNA and cells contained by the extraction of DNA and cells and the resulting fragment is inserted into a plasmid contained by the strength of the site cleaved with HindIII. This plasmid is transformed into E. coli as a host cell, colony hybridization is performed by the DNA probe method utilizing EcoRI fragments of pKUM1 and pKUM2 to select the bacterial cells containing a plasmid (pURR126) carrying the CG antigenic gene. E. coli JM 109 which comprises the plasmid CC pKUM1 or pKUM2 is deposited with FRI under accession No. FERM P-10318 CC 027A1319. The base sequence of the 46 kd antigen gene is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NIFL-) NIPPON FLOUR MILLS. Seto Y, Futo S, Mitsuse S, WPI; 92-089874/12.
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EP-475185-A.
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02-NOV-1992
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344
                           261 VKD------LRVLYDKLSVSIDSDIDSE
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KPDYVLGKVAVEVLRVLIAKKNKASRSEVENE
                                                                                                                                                                                                                                                                                       RWISAQKDIISYVDETEAATSTITKNQD-----AQNNW----LTQQANLSPAPLGFIIAPE 120
                                                      SKPASIFLGFLAPNDGMAEQAITKLKLEGFDTQKIFVTGQDYNDKAKTFIKDGDQNMTIY
                                                                                                               ----ELMKNSQNKIIDLSPEGENAVYVPGWNYGTAGQRIQSFLTINKDPAGGNKIKAVG
                                                                                                                                           FKGWADLIWSNPNYIPNISSR------
                                                                                                                                                                      LGKEDGAFDSIDOMNEYLKSHMPQETISFYTIAGS-----QDDNNSQYPYNGAMKVLK
                                                                                                                                                                                                  LGK--GLIDNIKIMKEI-------KVSVYSLGYEIDLEVLFEDMNGMEYAY--SMGTLK 202
                                                                                                                                                                                                                               --NGSGVGTAVNTIADKGIPIVAYDR---LITGSDKYDWYVSFDNGKVGELQGLSLAAGL 175
                                                                                                                                                                                                                                                          VVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFY----SGESGN-----QF
                                                                                   Similarity
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Pred. No. 0.
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Matches 64; Conserv
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W09851803-A1.

19-NOV-1998.

12-MAY-1998; U09629.

20-OCT-1997; US-062892.

16-MAY-1997; US-857884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents dispeptidyl aminopeptidase (DPAP) from Saccharomyces cerevisiae. DPAP acts synergistically with aminopeptidase (AP) to hydrolyse polypeptides, producing protein hydrolysate (PH), useful in foods as flavour enhancer, e.g. in baked goods, enriched in: (a) Ala, Arg, Asp, Gly and/or Val, or (b), if the substrate has been deamidated, in Glu (free and/or peptide bound), in which case products are useful as animal feed additives. DPAP can also be used in flavour-improving compositions (optionally containing AP) and in dough pre-mixes, also for deactivating enzymes and for converting precursors to mature proteins. DPAP increases the level of hydrolysis of proteins and thus of flavour development, and a mixture with AP may hydrolyse tripeptides that are resistant to either enzyme used alone. PH have improved solubility, emulsifying and foaming properties, and products containing them have better flavour, palatability, mouthfeel, aroma and crust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-1997; US-062892.
16-MAY-1997; US-857884.
(NOVO ) NOVO NORDISK BIOTECH INC.
Blinkovsky A, Brown K, Byun T, Klotz A, Rey MW;
WPI; 99-045232/04.
New dipeptidyl aminopeptidase from Aspergillus oryzae - used to
produce protein hydrolysates enriched in particular amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1999 (first entry)
Saccharomyces cerevisiae dipeptidyl aminopeptidase I.
Saccharomyces cerevisiae dipeptidase; protein hydrolysate; dough;
Prolyl dipeptidyl aminopeptidase; protein hydrolysate; dough;
flavour enhancer; palatability; mouthfeel; aroma; crust colour;
baking; animal feed additive; hydrolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as flavour enhancers, e.g. in doughs Example 7; Page 59-61; 77pp; English.
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NMNEAYLSDTKIKYPKPGFQN 411
                                                                                                                                          KKVTEDGSKDIFNAKPDWIYEEEVLASDQAIWWAPDDSKAVFARFNDTSVDDIR-LNRYT 390
                                                                                                                                                                                                                   -----KDL-----RVLYDKLSVSIDSDI-----DSESVFKVYETSGTESLRKLKAHE 303
                                                                                                                                                                                                                                                                                            GNIEPILPPEKSDDNYELGLSKL-----SYAHFSPAYNYIYFVYENNLFLQQVNSGVA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EFTVSTVQINYKLD-KLIFGTNLESEFRHSS-----KGF-----YWIKDLNT 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6%; Score 95.5; DB 1; Length 931; nilarity 19.9%; Pred. No. 0.91; Conservative 45; Mismatches 85; Indels 12
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Search completed: August 18, 1999, 17:36:37 Job time: 994 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

Š protein protein search, using sw model

Run August 18, 1999, 17:39:09; Search time 11.18 Seconds (without alignments) 1222.033 Million cell upda

cell updates/sec

Title: Perfect score: US-09-004-395-2 1719 1 MKRKAKSILFFLL

MKRKAKSILFFLLSTVLFAQ......FQNFVEKIESEKPEESSPKN 341

Scoring table:

122810 segs, 40065486 residues

PIR_60:* pir1:*
pir2:*
pir3:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

3 3	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	v	œ	7	σ	رب ر	4	w	N		NO.	DD0::1+
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S44168 B36590	F70177	S36773	A49737	T01408	\$46302	S38173	T00135	C64567	A33319	S57157	S61175	A56153	S14950	A69368	S54353	H71874	E71240	G70163	S06286	JC6033	B64710	A64494	A45515	A71298	JC5574	S14949	D69735	B70126	A41322	G64327	F64385	I40492	H71297	28	382	13	C70183	ID	
dnaK-type molecula dnaK-type molecula	transcription-repa		dipeptidyl aminope		plecul	ě	hypothetical prote	fucosyltransferase	microtubule-associ	hypothetical prote	probable membrane	46K surface antige	-	hypothetical prote	inter-alpha-inhibi	Ø	•	hypothetical prote	major merozoite su		-	hypothetical prote		probable flagellar	inter-alpha-trypsi	moleci		rface-located m	cetvlmuramov	H+-transporting AT	hypothetical prote		0		eríplasmic	н	qe1		

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#### ALIGNMENTS

RESULT 1

C70183

C70183

C70183

C70183

C;Species: Borrelia burgdorfer1 (Lyme disease spirochete)

C;Species: Borrelia burgdorfer1 (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998

C;Accession: C70183

C;Accession: C70183

C;Accession: C70183

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943

A;Accession: C70183 8 Z S

A;Molecule type: DNA A;Restdues: 1-344 <KLE> A;Cross-references: GB:AE001168; GB:AE000783; NID:g2688598; PID:g2688608; TIGR:BB0668 A;Experimental source: strain B31 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

Query Match 99.0%; Best Local Similarity 98.8%; Length 344;

Š Matches Conservative Score 1701; DB 2; Pred. No. 9.3e-120; 2; Mismatches 2; Indels Gaps 0

á В 

밁 64

& Š 124 121 LGVRVLPPSYSQSSAMIMPPPKIPFYSGESGNQFLGKGLIDNIKTMKEIKVSVYSLGYEI 183 LGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKGLIDNIKTMKEIKVSVYSLGYEI 180

밁 Qy 184 181 DLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMR DLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMR 240 243

Ş 241 FKAFRYSKSHSSKVKNFIFYVKDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLK 300

밁 244 FKAFRVSKSHSSKEQNFIFYVKDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLK 303

301 AHETFKRVLKLREKISIAEGSFQNFVEKIESEKPEESSPKN 341

AHETFKRVLKLREKISMPEGSFQNFVEKIESEKPEESSPKN 344

304

protein

flagellar fllament outer layer protein flaA-1 precursor - syphilis spirochete N;Alternate names: 37K endoflagellar sheath protein FlaA; minor endoflagellar processes: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999 C;Accession: D71348; A40160; A37187; B27559; A32351 R;Fraser; C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998

**3** 0

sequence of Treponema pallidum, the syphilis spirochete

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RISAACS, R.D.; Hanke, J.H.; Guzmaurrung.

RISAACS, R.D.; Hanke, J.H.; Guzmaurrung.

A;Title: Molecular cloning and DNA sequence analysis of the 37-kilodalton A;Reference number: A37187; MUID:90035409

A;Accession: A37187

A;Status: preliminary

A;Molecular type: DNA

A;Residues: 21-350 <ISA2>

A;Cross-references: GB:M26525; NID:g155056

A;Cross-references: GB:M26525; MID:g155056

A;Cross-references: GB:M26525; MID:g155056

A;Cross-references: GB:M26525; MID:g155056

A;Cross-references: GB:M26525; MID:g15056
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A;Accession: B27559
A;Molecule type: protein
A;Residues: 21-28,'X',30-36,'G',38-40 <BLA>
R;Norris, S.J.; Charon, N.W.; Cook, R.G.; Fuentes, M.D.; Limberger, R.J.
Bacceriol. 170, 4072-4082, 1988
A;Title: Antigenic relatedness and N-terminal sequence homology define two
A;Reference number: A91882; MUID:88314903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Blanco, D.R.; Champion, C.I.; Miller, J.N.; Lovet Infect: Immun. 56, 168-175, 1988
A;Title: Antigenic and structural characterization A;Reference number: A91753; MUID:88085470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Experimental source: strain Nichols R:Isaacs, R.D.; Radolf, J.D. Infect. Immun. 58, 2025-2034, 1990 A:Title: Expression in Escherichia coli of A:Reference number: A40160; MUID:90307197 A:Accession: A40160
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A;Accession: D71348
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R;Isaacs, R.D.; Hanke, J.H.; Guzman-Verduzco, L.M.; Newport,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-29 <ISA1>
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                                   SVFKVYETSGTESLRKLKAHETFKRVLKLREKISIAEGSFQNFVEKIESEK
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Pred. No. 8e-20;
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A; TITLE: Cloning and DNA sequence a A; Reference number: A43824; MUID:92 A; A; Accession: A43824
                                                                                                                                          G.Accession: A.J.
R;Brahamsha, B.; Greenberg, E.P.
J. Bacteriol. 171, 1692-1697, 1989
A;Title: Cloning and sequence analysis of
A;Title: A32814; MUID:89155480
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A; Residues:
C; Keywords:
                                                                                                                                A; Reference number: A32814;
A; Accession: A32814
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C;Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change
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A; Residues: 1-320 < KOO>
                                 A; Molecule type: DNA
A; Residues: 1-301 <B
                                                                                              A; Status: preliminary;
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Query Match Best Local S Matches 57

ch 11.8%; 1 Similarity 31.0%; 57; Conservative

32;

Score 202.5; DB 2; Pred. No. 4.7e-08; 2; Mismatches 68;

2;

Length Indels

301;

27;

Gaps

7;

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A; Status; rac---
A; Molecule type: DNA
A; Residues: 1-242 <COL>
A; Cross-references: GB: AE001240; GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable outer membrane protein - syphilis spirochete
(;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999
C;Accession: H71297
R;Fraser; C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
 gntR-type transcription regulator homolog ycxD - Bacillus
N;Alternate names: hypothetical protein 8 (srfA operon)
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_c
C;Accession: I40492; F69766; S34990
R;Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Pe
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Matches
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                                                                                                                                                                                                                                                                                                              GKGLIDNIKTMKEIKVSVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPN
                                                                                                                                                                                                                                                                                                                                            MPQAVRMAGSWQGKDKEARFIGVECKFNRQGNNWLDLIPTKGGSDYEIPLRGVVSG----
                                                                                                                                                                                                                                                                                                                                                                                                         PLAAQRSKVNYQAYFIDDFDGAS------EDQGL-AWRAAGSKFITKGFPILKYFEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSTRLDLTNYVDYV---YSGASGIVKPEDMVVDLGINNW----SVLLTPSARLQAYVKN 100
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                                                                                                                                                            NMHID
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                                                                                                                                                                                                                                                                                                                                                                           SVVAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIMP-----PFKIPFYSGESGNQFL 155
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Pred. No. 0.038;
1; Mismatches 105;
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                                 12-Aug-1996 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not shown;
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    M.; Venema, G.;
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RESULT 7
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R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, R; Reich, C.I.; Overbeek, R.; Kirkness, E.F.;
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A;Experimental Source: ATCC 21332

A;Experimental Source: ATCC 21332

C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.;

A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C.; Ferrari,

A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C.; Ferrari,

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino,

A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl

A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A; Authors: Yoshikawa, H.F.; Zumsteln, E.; Yoshikawa, H.; Danchin, A.

A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

A; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: ycxD
C; Superfamily: hypothetical protein b1439
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A; Residues: 1-444 < KUN>
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A; Residues: 1-444 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence
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                                                                 SESVEKVYETSGTESLRKLKAHETEK-RVLKLREKI----SIAEGSF
                                                                                                                                                                                                                                                                  ERDKQ----
                                                                                                                                                                                                                                                                                                                             DNIKTMKEIKVSVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPNYIPNI
SQAALEIYLKSGMYGRHKEKIRDSYKERSLRLHQAIRTHRQLGSGRF
                                                                                                                                                                                             SSRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKVKNFIFYVKDLRVLYDKLSVSIDSDID
                                                                                                                                                                                                                                                                                                                                                                                                  TLGIPAIGVKRTEE--GLDIAKVERLFQTESIKFFYTMPRFHNP-----LGCSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVVAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKGLI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKSGQPGP--IDFATSAPDP-----DVFPYLDFQHCINKAIDTYKNDLFIYGTPKGLPSL 125
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                                                                                                                            SSHVI-----YLKSFSKMMFPGLRVGAAVLPEALTDTFYA-----YKKLN-DIDCSMI
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                                                                                                                                                                                                                                                                  - ELVRLAEAYDVYLVEDDY - - -
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368
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#sequence_revision 13-Sep-1996 #text_change 10-Oct-199;

jannaschii

G.J.; Zhou, L.; Fleischmann, Frkness, E.F.; Weinstock, K.G.;

R.D.; Merrick,

Sutton, G. ick, J.M.;

Glodek,

```
H+-transporting ATP synthase (EC 3.6.1.34) subunit I - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13:Sep-1996 #sequence_revision 13:Sep-1996 #text_change 10:Oct-1997 C;Accession: G64327 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake R; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch, A;Reference number: A64300; MUID:96337999
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococ A;Reference number: A64300; MUID:96337999
                                                                                                                                                                                                                                                                            A:Map position: REV214151-212064
A:Start codon: GTG
C:Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                               A:Molecule type: DNA
A;Residues: 1-695 <BUL>
A:Cross-references: GB:U67478; GB:L77117;
C:Genetics:
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G64327
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A;Map position: REV615409-613667
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A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA
A;Residues: 1.580 <BUL>
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A;Accession: G64327
A;Status: preliminary; nucleic acid sequence
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                                                                     32
                                                                                                              GIVKPEDMVVDLGINNWSVLLTPSARLQAYVKNSVVAPAVVKSESKRYAGDTILGVRVL- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REKISIAEGSFQNFVEKI 329
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                                                                   GIVELCDLSEKLEDLEWKTLLSPSSSAD-YVRN--VTSLMIK-----AG-----RILD
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23.5%; Pred. No. 2.2;
tive 41; Mismatches
-MPPFKIPFYSGESGNQFLGKGL--
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Pred. No. 1.3;
38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    NID:g1590958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          not shown; translation
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; Glodek, A.;
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KARGDAYSQFGKTDRTYYIEAWVPARDAEKAKSLIENSADGFAFVEITEPDEPEEKIP
                                                                              -----SDVEGTPSEALSKIESELKAIESERNSLIEKLKALAQKWEKELLAVYELLSIE 292
                                                                                                                                                                                                   WSNPNYIPNIS-SRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKVKNFIFYVKDLRVLYD 269
                                                                                                                                                                                                                                                                                  NIKT-MKEIKVSV-YSLGYEIDLEVLFEDMNGMEYAY-----SMGTLKFKGWADLI 210
                                                                                                                       KLSVSIDSDIDS-----
                                                                                                                                                               KVADGYIGIFSGSEFEKDKKIRVPIVFVTLKEKLENV ---- LSEIRKFEFERYDI ---- 240
                                                                                                                                                                                                                                              NKKSKLLQLKEQISYLKGLEFDLKYL----GSGEYVFIGAGSVPKEKLGELK----AELD 188
                                                                                                                                                                                                                                                                                                                             MFSSVSQKETSIKDILNPKPVEKKKVSFNSYQEVIDYAEKVLNEISKEVDGPAERLSELD 136
                                                                                                                     -ESVFKVYETSGTESLRKLK--AHETFKRVLKLREKISI- 318
                                        ----AEGSFQN-----FVEKIESEKPEESSP 339
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C;Species: Bacillus subtills C;Date: 05-Jun-1992 #sequence_revision C;Accession: A41322; C47679; D69654 R:Kuroda, A.; Sekiguchi, J.
Bacteriol. 173, 7304-7312, 1991
A:Title: Molecular cloning and sequencing
A:Reference number: A41322; MUID:92041629
A:Accession: A41322
A:Molecule type: DNA
A:Residues: 473-705 < KUR> A;Title: Sequencing and analysis of the Bacillus subtilis lytRABC divergon: a regulat A;Reference number: A47679; MUID:93018998
A;Accession: C47679 N-acetylmuramoyl-L-alanine amidase modifier precursor lytB - Bacillus subtilis N; Alternate names: major autolysin lytC modifier lytB; probable cell wall-binding 10-Feb-1995 #text_change 24-Sep-1998 Karamata, of a major Bacillus subtilis autolysin gene

A; Molecule type: DNA A; Residues: 1-705 <LAZ> R;Lazarevic, V.; Margot, P.; Soldo, B.; J. Gen. Microbiol. 138, 1949-1961, 1992 A; Cross-references: GB:M61747

A;Crossreferences: GB:M87645; NID:g143155; PID:g143158
A;Crossreferences: GB:M87645; NID:g143155; PID:g143158
A;Experimental source: strain 168
A;Experimental source: strain 16

A;Accession: D69654

Status: preliminary; nucleic acid sequence not shown; translation

A;Residues: type: DNA : 1-705 <KUN>

not

A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PID:e1184469; PID:g2636089 A;Experimental source: strain 168 C;Comment: This protein enhances the activity of the N-acetylmuramoyl-L-alanine amid amida

A;Gene: lytB

<SIG>

A;Start codon: TTG C;Keywords: cell wall E;1-25/Domain: signal sequence #status predicted <SIG E;26-705/Product: N-acetylmuramoyl-L-alanine amidase modifier #status predicted <MAT>

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Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943

A;Accession: B70126
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Residues: 1-1119 <KLE>
A;Cross-references: GB:AE001131; GB:AE000783; NID:92688098; PID:92688100; TIGR:BB0210
A;Experimental source: strain B31
C;Superfamily: tetratricopeptide repeat homology
F;742-774/Domain: tetratricopeptide repeat homology <TT3>
F;803-847/Domain: tetratricopeptide repeat homology <TT3>
F;813-875/Domain: tetratricopeptide repeat homology <TT3>
F;911-943/Domain: tetratricopeptide repeat homology <TT3>
F;111-1044/Domain: tetratricopeptide repeat homology <TT3>
F;111-1044/Domain: tetratricopeptide repeat homology <TT3>
F;111-1044/Domain: tetratricopeptide repeat homology <TT3>
F;1011-1044/Domain: tetratricopeptide repeat homology <TT3>
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surface-located membrane protein 1 (lmp1) homolog - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998
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Best Local S
Matches 68
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  97
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                                                                                                                                                                                                                     Match 6.1%;
Local Similarity 21.7%;
les 68; Conservative 44
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                                                                                                   VKNSVID----RNYKKAYS-----VAKLLQDKYPQNEDIAMLTNTLAEIANSSPFESKDL
                                                                                                                                                              VKNSVVAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIM------PPFKIPFY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVKQDSVPAAAKSITKDKATYAYDFI-----GSTSSISAEVENSLADEFYLADGGTYN
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QRDSANQILDKIKGQ-DNTKTNVNENFDIAFNNRYIKDSTITENYSDRNDDVGIEDEDIS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLKAHETFKRVLKLREKISIAEGS 321
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                                              SGESGNQFLG--KGLIDNIKT-------MKEIKVSVYSLGY-EIDLEVLFEDMNGM 192
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25.1%; Pred. No. 2.7;
                                                                                                                                                                                                                     ; Score 104.5; |
; Pred. No. 6.2;
44; Mismatches
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Vugt,
B.
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5 B 5

349

DSSIRGSLIGMDGAHNRKHFLRAIMEGITFSLHESIELFREAGKSVHTVVSIGGGAKNDT

-SKYKNFIFYVKD-----LRVLYDKLSVSIDSDID-----SESVFKVYETSG---TES

SFXTMGVTLAAGYS-LDWFKRTFAPNESFEQLLQGVEAIPIGANGLLYTPYLVGERTPHA

251 348

YAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDDVPNYPLASSKMRFKAFRVSK--SHS

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RESULT 11
D69735

xylulose kinase xylB - Bacillus subtilis
C;Species: Bacillus subtilis
R;Kunst, A.; Alloni, G.; Ran, A.; Fullori, A.; Alloni, G.; Ran, S.; Caldvell, B.; Fullor, J.; Fabret, C.; Ferrari,
A;Authors: Cscheich, G.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sakowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Atcession: D69735
A.;Cession: D697
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A; Molecule type: DNA
A; Residues: 1-499 <KUN>
A; Cross-references: GB: Z99113; GB: ALO09126; NID: g2634090; PID: e1183420; PID: g2634145
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C;Superfamily: xylulokinase
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                                                                                                                                                                                                                                                                                                                           141
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                                          KIPFYSGESGNQ--FLGKGLIDNIKTMKEIKVSVYSLGYEIDLE-----VLFEDNNGME 193
                                                                                                                                                                                                                                                                                                                       KEHEP-ELFKKTAVFLLPKDYVRFRMTGVIHTEYSDAAGTLLLHITRKEWSNDICNQIGI 199
                                                                                                                                                                                                                                                                                                                                                                                                       KRAEPGELVLDFAELARDPSSTRLDLTNYVDYVYSGASG----IVKPE---DMVVDLGI 81
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KTKVYAGGADNACGAIGAGILSSGKTLCSIGTSGVILSYEEEKERDFKGKVHFFNHGKKD
                                                                                                                                                                                                                                       NNWSVLLTPSARLQAYVKNSVVAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPF 141
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                                                                                                                                                                -----CVGSLLPHVAAKTGLLE---
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289
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C;Function:
A;Description: i
C;Superfamily: f
C;Keywords: ATP;
         inter-alpha-trypsin inhibitor heavy chain 1 - golde C; Species: Mesocricetus auratus (golden hamster) C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 C; Accession: JC5574; PC4484 R; Nakatani, T; Suzuki, Y; Yamamoto, T; Sinohara, J. Biochem. 122, 71-82, 1997 A; Title: Molecular cloning and sequencing of cDNAs sin inhibitor heavy chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
S14949
dnaK-type
                                                                                                                                   RESULT
JC5574
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C;Genetics:
A;Gene: hsc-1
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A;Title: Sequences of two hsc 70 cDNAs from Lyc A;Reference number: $14949; MUID:91370894
A;Accession: $14949
A;Molecule type: mRNA
A;Residues: 1-650 <LIN>
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Best Local S
Matches 68
inhibitor heavy chain feference number: JC5574;
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                                                                                                                                                                                                                                                                                 SDIDSESVFKVYETSGTESLRKLKAHETFKRVLKLREKISIAEGSFONFVEKIESEKPEE
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68; Conserv
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 MUID: 97420688
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Pred.
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                           encoding three
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                           heavy-chain precursors
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142 KIPFYSGESGNQFLGKGLIDNIKTM-----KEIKVSVYSLGYEIDLEVLFEDMNGMEYA 195

KVSFYR-RGYNSF----EVSSVKPLPVEGVAKTVSVWVAGRGYPHSLSLLLEDFWGQRFE 153

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R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, larson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, They, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A;Reference number: A71250; MUID:98332770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Molecule type: protein
A; Residues: 387-400; 461-475 < NA2>
C; Comment: In the plasma three inter-alpha-trypsin inhibitor heavy
that the complexes play important role for panceatic cancer.
C; Superfamily: inter-alpha-trypsin inhibitor complex component II
F; 247-250,690-890/Disulfide bonds: #status predicted
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-914 <NAK>
A;Cross-references: DDBJ:D89285; NID:g1694687; PID:d1014635; PID:g1694688
A;Experimental source: liver
A;Accession: PC4484
A;Accession: PC4484
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-241 <COL>
                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: A71298
                                                                                                                                                                                                                                                                                                                                                                                                                       probable flagellar filament outer layer protein (flaA-2) - syphilis spirochete c;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999 C;Accession: A71298
                                                                                                                   A; Gene:
                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                            A; Experimental source:
                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence
                                                                                                                 Genetics:
Gene: TP0664
                           Query Match
Best Local Similarity
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59; Mismatches
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R;Lee, M.G.S.; Polvere, R.I.; Van der Ploeg, L.H.T.
MOL. Blochem Parasitol, 41, 213-220, 1990
A;Title: Evidence for segmental gene conversion between a cognate hsp70 gene and the tem
A;Reference number: A45515
A;Recession: A45515
A;Status: preliminary
A;Molecule + troc. ****
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N;Alternate names: heat shock-related protein
C;Species: Trypanosoma brucei
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 13-Mar-1998
C;Accession: A45515
R;Lee, M.G.S.; Polyere, R.I.; Van der ploeg, L.H.T.
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A;Residues: 1-676 <LEE>
A;Cross-references: GB:M32139; NID:g162124; PID:g162125
C;Function:
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## GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 1999, 09:33:06; Search time 10.76 Seconds (without alignments) 895.863 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-004-395-2 1719 1 MKRKAKSILFFLLSTYLFAQ......FQNFVEKIESEKPEESSPKN 341

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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IGNAL. FLAG 7 MW; B6	SWISCELLULAR LOCATION: PERIPLASMIC FL. SWISS-PROT entry is copyright. It is een the Swiss Institute of Bioinfor European Bioinformatics Institute. by non-profit institutions as loon fied and this statement is not remove ties requires a license agreement (Seend an email to license@isb-sib.ch).	DENCE OF 22-49.  NAIN=M.;  NAIN=M.;  NAIN=M.;  SAIN=M.;   SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 89155480. BRAHAMSHA B., GREENBERG E.P.; TCloning and sequence analysis of flaA, a aurantia flagellar filament surface antig. J. BACTERIOL. 171:1692-1697(1989). [2] [2] REVISIONS. GREENBERG E.P.; SUBMITTED (JAN-1991) TO EMBL/GENBANK/DDBJ	PED) SEQUENCE ANNO ANNO ANNO ANNO ANNO ANNO ANNO ANN	ALIGNME	
FLAGELLAR FILAMENT B6AE70C3 CRC32;			flaA, a ge ce antigen.	RT; 337 AA JENCE UPDATE) JENTION UPDAT PROTEIN PREC PROTEIN PREC	ALIGNMENTS
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FLAA_TREPA
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                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and institutions are not removed.
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MEDLINE; 98332770.

FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON (
DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
EMBL;
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                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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01-CCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
FLAGELLAR FILAMENT OUTER LAYER PROTEIN PRECURSOR (SHEATH PROTEIN).
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ISAACS R.D., RADOLF J.D.;
Expression in Escherichia coli of the sheath protein of Treponema pallidum by reaction and a T7 expression system.";
INFECT. IMMUN. 58:2025-2034(1990).
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AE001206;
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RESULT 3
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FLAGELLA; PERIPLASMIC; SIGNAL 20
CHAIN 21 350
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01-OCT-1993 (REL. 2
01-OCT-1993 (REL. 2
15-JUL-1998 (REL. 3
                                   KOOPMAN M.B.H., BAATS E., VAN VORSTENBOSCH C.J.A.H.V.,
VAN DER ZEIJST B.A.M., KUSTERS J.G.;
"The periplasmic flagella of Sepulina (Treponema) hyodysenteriae
composed of two sheath proteins and three core proteins.";
J. GEN. MICROBIOL. 138:2697-2706(1992).
1- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
-!- SUBUNIT: OUTER LAYER IS COMPOSED OF TWO SHEATH PROTEINS, FLAA1
(44 KD) AND FLAA2 (35 KD) AND A CORE THAT CONTAINS THREE PROTE
FLAB1 (37 KD), FLAB2 (34 KD) AND FLAB3 (32 KD).
                                                                                                                                                                                                                                                                            SEQUENCE C
STRAIN-C5;
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COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., KUSTERS COOPMAN M.B.H., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., DE LEEUW O.S., VAN DER ZEIJST B.A.M., KUSTERS COOPMAN M.B.H., LEEUW D. C. LEEUW D.
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27, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
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20 POTENTIAL.
20 FLAGELLAR F
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28.5%;
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SPIROCHAETACEAE; BRACHYSPIRA
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9 CRC32;
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                                                      COSMINA P., RODRIGUEZ F., DE FERRA F., VENEMA G., VAN SINDERN D.;
"Sequence and analysis of the genetic synthesis in Bacillus subtilis.";
                                                                                                                                                                                                                                                YCXD_BACSU
Q08792;
                                                                                                 STRAIN=168 / JH642;
MEDLINE; 93360813.
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                BACTERIA;
                                                                                                                                                                           BACILLUS SUBTILIS
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01-NOV-1997
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                                             MOL. MICROBIOL.
            STRAIN-168
                     SEQUENCE FROM N.A
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                                             8:821-831(1993)
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31, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
KD PROTEIN IN SRFA4-SFP INT
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                                                                                        DE FERRA F.,
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Q58099;
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01-NOV-1997
01-NOV-1997
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SEQUENCE
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EMBL; D50453; G1805428; -.
EMBL; D50453; E1182308; -.
EMBL; Z99105; E1182323; -.
SUBTILIST; BG10175; YCXD.
PFRAM; PF00392; gntR; 1.
HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
SEQUENCE FROM N.A. STRAIN-JAL-1 / DSM MEDLINE; 96337999.
                                                                                                                        METHANOCOCCUS JANNASCHI
ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The 25 degrees-36 degrees region of the Bacillus chromosome: determination of the sequence of a 14 identification of 113 genes."; MICROBIOLOGY 142:3047-3056(1996).
                                                                                                     METHANOCOCCUS
                                                                                                                                                                                                     HYPOTHETICAL
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BINDING 286 2
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Pred. No. 0.
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                                                                                                                             METHANOCOCCACEAE;
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IPI_METJA STANDARD;

D ATPI_METJA STANDARD;

C 057675;

OT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

""""""""" """" (EC 3.6.1.34).
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGGYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOCHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
                                                                                                  STRAIN=JAL-1 / DSM 2661
MEDLINE; 96337999.
                                                                                                                                                                                      METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL
SEQUENCE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67515; TIGR; MJ0686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCIENCE 273:1058-1073(1996).
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                        METHANOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                               567
                                                                                                                                                                                                                                                                                                                                                                                                                                              312
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                                                                                                                                                                                                                                                                                                                                                                                                                                              REKISIAEGSFQNFVEKI 329
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21.7%;
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                                                                                                                                                                                       METHANOCOCCALES; METHANOCOCCACEAE;
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                                                                                                                     ATCC
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Pred.
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No. 1
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RRROCOGEDIA
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LYTB_BACSU
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Best Local S
Matches 84
                                                                                                                                                         01-JUL-1993 (REL. 26, CREATE O1-JUL-1993 (REL. 26, LAST S. 01-FEB-1995 (REL. 31, LAST AL AMIDASE ENHANCER PRECURSOR (MLYTB OR CWBA. BACILLING CONTROL OF C
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SEQUENCE
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Q02113;
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SCIENCE 273:1058-1073(1996).
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SEQUENCE FROM STRAIN=168;
                                                                                    BACILLUS
                                                                                                                            BACTERIA; FIRMICUTES;
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HYDROLASE; HY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270
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84; Conservative
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                                                                                                                            BACILLUS/CLOSTRIDIUM GROUP;
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ANNOTATION UPDAT
(MODIFIER PROTEI
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Pred. No. 1.9;
1; Mismatches
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Best Local S
Matches 76
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SIGNAL 25 25
CHAIN 26 705 AM
DOMAIN 64 349 3 3
REPEAT 162 251 2.
REPEAT 252 349
SEQUENCE 705 AA; 76729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUNDDA A., RASHID H.M., SEKIGUCHI J.;

KUNDDA A., RASHID H.M., SEKIGUCHI J.;

Wolecular cloning and sequencing of the upstream region of the major Bacillus subtilis autolysin gene: a modifier protein exhibiting sequence homology to the major autolysin and the spoild product.";

J. GEN. MICROBIOL. 138:1067-1076(1992).

-i. FUNCTION: POSSIBLY INVOLVED IN CELL WALL METABOLISM DURING SPORE FORMATION. ENHANCES THE AMIDASE ACTIVITY APPROXIMATELY THREEFOLD.

-i. SUBCELLULAR LOCATION: MEMBRANE-BOUND.

-i. SUBCELLULAR LOCATION: MEMBRANE-BOUND.

-i. SUBCELLULAR SPOILD GENE AT ITS C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Sequencing and analysis of the Bacillus subtilis lytraBC divergon:
regulatory unit encompassing the structural genes of the N-
acetylmuramoy1-L-alanine amidase and its modifier.";
J. GEN. MICROBIOL. 138:1949-1961(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z99122; E1184469; -. PIR; C47679; C47679.
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LAZAREVIC V., MAR
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                                                                                                                                                         KDLRVLYDKLSVSIDSDIDSESVFKVYETSGTESLRKLKAHETFKRVLKLREKISIAEGS
                                                                                                                                                                                                                                                                                                                                LKINSGKLNLENIKTYGNSLRIKPENYSTSNRISLD-----GKQY---LGTVNFS---
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Pred. No. 2.3;
32; Mismatches
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3 X TANDEM REPEATS
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
115-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1
CHAIN H1).
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            GLYCOPROTEIN.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
APTTONACTYLA: SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 CHAIN
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-----VQSWRGSLVQASTANLDAARSYVRQFSLA-----GSTNLNGGLLRGIEIL
                                                 PEDMYVDLGINNW--SVLLTPSARLQA---YVKNSVVAPAVVKSESKRYAGDTILGVRVL
                                                                                              LLSTVLFAQETDGLAEGSKRAEPGELVLDFAELARDPSSTRLDLTNYVDYVYSGASGIVK
                                                                         LNKNVVFVIDISSSMEGQKVKQTKEALLKIL-----SDLKPGDYFDLVLFGSA----
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EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                        WE;
                                                                                                                   61;
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                                                                                                                  Score 105; DB:
Pred. No. 3.4;
61; 'Mismatches'
                                                                                                                                                                     POTENTIAL.
E -> D (IN REF. 2).
R -> M (IN REF. 2).
S -> A (IN REF. 2).
W -> G (IN REF. 2).
C -> S (IN REF. 2).
C -> S (IN REF. 2).
VR -> SV (IN REF. 2).
L -> V (IN REF. 2).
L -> V (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
I -> Y (IN REF. 2).
I -> Y (IN REF. 2).
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                                                                                                                                      Length 902;
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Best Local S
Matches 68
                                                                                                                                                           PFAM; PF00370; FGGY;
TRANSFERASE; KINASE;
SEQUENCE 499 AA; 5
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01-NOV-1997 (REL. 35, LAST ANOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANOTATION UPDATE)
XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE).
                                                                                                                                                                                                      PROSITE; PS00445; FGGY_KINASES_1; PROSITE; PS00933; FGGY_KINASES_1;
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEIC ACIDS RES. 13:5717-5722(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of the Bacillus subtilis xylose isomerase gene: extensive homology between the Bacillus and Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
BORCHERT S., KLEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P39211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILHELM M., HOLLENBERG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
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                              141
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 82
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                                                                                                                                                                                                                                                                                                                                                                                                                       5-PHOSPHATE.
SIMILARITY: BELONGS TO THE FUCOKINASE /
GLYCEROKINASE / XYLULOKINASE FAMILY.
                                            KRAEPGELVLDFAELARDPSSTRLDLINYVDYVYSGASG----IVKPE---DMVVDLGI 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGDQGFKTTCLVDEEEMKKLLQERGHMLENYVERLWAYLTIQELLAKRMKLEWAE
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NNWSVLLTPSARLQAYVKNSVVAPAVVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPF 141
                                KEHEP-
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                                                                                                    Similarity
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                           ELFKKTAVFLLPKDYVRFRMTGVIHTEYSDAAGTLLLHITRKEWSNDICNQIGI 199
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                                                                                       Conservative
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                                                                                                                                                             ; XYLOSE METABOLISM.
55417 MW; 1E3E31A1
                                                                                                    6.1%;
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DEMBL/GENBANK/DDBJ DATA I
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קי
                                                                                       57;
                                                                                                    Score 104;
Pred. No. 1
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                                                                                       Mismatches
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                                                                                                                                                              CRC32;
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IPFYSGESGNQFL-GKGLIDNIKTMKEI-KVSVYSLGYEIDLE----

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RESULT 10
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ID HS71_DT 01-MAR--
DT 01-MAR--
DT 01-MAR--
DT 01-CT--
CC EUPKAYZOO
CC EUPKYLLO
CC ASTERIDA
RN HSTERIDA
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PROSITE; PS00297; HSP70_2; 1.

PROSITE; PS00329; HSP70_3; 1.

PROSITE; PS01036; HSP70_3; 1.

PFAM; PF00012; HSP70; 1.

HSSP; P19120; 1MGI.

ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.

SEQUENCE 650 AA; 71287 MW; 98C96C58 CRC32;
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LIN T.Y., DUCK N.B., WINTER J., FOLK W.R.;

"Sequences of two hac 70 cDNAs from Lycopersicon esculentum.";

PLANT MOL. BIOL. 16:475-478(1991).

-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.ieh-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-MAR-1992 (REL. 21,
01-OCT-1996 (REL. 34,
HEAT SHOCK COGNATE 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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18.8%;
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Best Local S
Matches 66
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1 |
CHAIN H1).
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00092; vwa; 1.
SERINE PROTEASE INHIBITOR;
GLYCOPROTEIN.
                                                                                                                                                                                                                                                     EMBL; D89285; D1014635; -. PFAM; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MESOCRICETUS AURATUS (GOLDEN HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RODENTIA; SCIUROGNATHI; MURIDAE; CRICETINAE; MESOCR:
                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                               VLFAQETDGLAEGSKRAEPGELVLDFAELARDPSSTRLDLTNYVDYVYSGASGIVKPED-
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                        LVFVIDISGSMEGQKVKQTKEALLKIL--
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 ---MVVDLGINNWSVLLTPS--ARLQA---YVKNSVVAPAVVKSESKRYAGDTILGVRVL 126
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914 AA;
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                                                                     Score 102.5; D
Pred. No. 5.3;
59; Mismatches
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RESULT 12

HS7C_TRYBB STANDARD; PRT; 676 AA.

ID HS7C_TRYBB STANDARD; PRT; 676 AA.

AC P20030;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)

DT 01-FEB-1991 (REL. 22, LAST ANNOTATION UPDATE)

DE HEAT SHOCK COGNATE HSP70 PROTEIN.

OS TEXPANOSOMA BRUCEI BRUCEI.
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Best Local Similarity 23.3
Matches 73; Conservative
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PEAM; PF00012; HSP70; 1.
HSSP; P19120; INGJ.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
ATP-BINDING; HEAT 3694 MW; 489ECDAF CR
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PIR; A45515; A45515.
PROSITE; PS00297; HSP70_1;
PROSITE; PS00329; HSP70_2;
PROSITE; PS01036; HSP70_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 90377290:
LEE M.G.-S., POLVERE R.I., VAN DER PLOEG L.H
"Evidence for segmental gene conversion betw
and the temperature-sensitively transcribed
Trypanosoma brucel.";
MOL. BIOCHEM. PARASITOL. 41:213-220(1990).
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23.2%; Pred. No. 4.2;
tive 44; Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 96337999.

BOLT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAIME B.P., BORDDOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschil."
                                                                                                                                                                                                                                                                                           CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=JAL-1 / DSM 2661 / ATCC MEDLINE; 96337999.
                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                        EMBL; U67596; G1500447; -. TIGR; MJ1554; -.
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YAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYS-----
                                                          D-----YYYSGASGIVKPEDMYVDLGINNWSVLLTPSARLQAYVKNSVVAPAYVKSESKR
                                                                                                              MKIKAVAIFLSLLMIISLFS----GCVENEKPIKEGS--NDFKLIPVNSKSNFEEFKNTV
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                                    ENSIGNYIYVGHSYASREVQITSTVKSSN----VETSTEPERFSKTNVQVKGVDEADILK
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77; Conserv
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622 AA;
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PROTEIN N
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                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                   POTENTIAL.
HYPOTHETICAL PROTEIN MJ1554.
; D24A84CB CRC32;
                                                                                                                                                                                                               Score 101.5;
Pred. No. 3.
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P19598; Q25921;
01-FEB-1991 (REI
01-NOV-1997 (REI
                   TRANSMEM
CARBOHYD
CARBOHYD
                                                                         SIGNAL
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                                                                                                                                                                             PIR;
                                                                                                                                                                                         EMBL; M35727; G160550; -. EMBL; Y00087; G9925; -. EMBL; Z35326; G535248; -.
                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSP-1.
PLASMODIUM FALCIPARUM
EUKARYOTA; ALVEOLATA;
   CARBOHYD
                                                                                                                   MALARIA; MEROZO TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             merozoite surface antigen-1.";
EXP. PARASITOL. 81:47-54(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A naturally occurring gene encoding the major suprecursor p190 of plasmodium falciparum lacks triemBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (REL.
01-NOV-1997 (REL.
MEROZOITE SURFACE
                                                                                                                                                         PFAM; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1032-1682 FROM N.A. MEDLINE; 95354793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PMMSA)
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                                                                                                                   MEROZOITE; POLYPROTEIN; REPEAT; BRANE; GPI-ANCHOR.
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233
462
528
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(REL. 35, LAST SEQUENCE UPDATE)

(REL. 35, LAST ANNOTATION UPDAT

(REACE PROTEIN 1 PRECURSOR (MERC
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                                                                             POTENTIAL.
MEROZOITE
                     MEMBRANE ANCHOR (POTENTIAL).
POTENTIAL.
POTENTIAL
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(MEROZOITE
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                                                                               SURFACE
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                                                                                                                                   SIGNAL; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r surface antigen tripeptide repeats.";
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Best Local
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CARBOHYD
CARBOHYD
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CARBOHYD
                                                                      SEQUENCE FROM N.A.

STRAIN-C57BL/6N; TISSUE-LIVER;

STRAIN-C57BL/6N; TISSUE-LIVER;

STRAIN-C57BL/6N; TISSUE-LIVER;

STRAIN-C57BL/6N; TISSUE J.D.;

The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein with differential transcription in liver and brain.";

BICCHEM. J. 306:505-512(1995).

FIGURE J. SUBUNIT: INTER-ALPHA-TRYPSIN INHIBITOR CONSIST OF A LIGHT OF A SUBUNIT.
  the Euro
                                                                                                                                                                                                                                                    15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1 PRECURSOR (ITI HEAVY CHAIN H1).
                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                             ITIH1
                                                                                                                                                                                                                                                                                                                                TH1_MOUSE
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                                                 SIMILARITY: BELONGS TO THE ITIH FAMILY.
  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                             ---LKKNENIKKLLEDIDKI-----KIDAEKP 320
                                                                                                                                                                                                                                                                                                                                                                                                                     LRKLKAHETFKRVLKLREKISIAEGSFQNFVEKIESEKP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAFRVSKSHSSKVK-----NFIFYVKDLRVLYDKLSVSIDSDIDSESVFKVYETSGTES
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RVDYYLIYSDIEGVKKSLDSLKHLIESYLVDEFNVKEELKKLADEEIKDVDLDSNFVLN
DNEDETEDEISDLLLEVENOKLFKVRLDFYKDNPMATISGLOMIQALKGLGKIFKSIP
DSSELLADKFFDFVIYYLISNTSEESIAKKINLPDVVSHFEIKNVNLESLKSVRLKED
DEAPFKENKNIKKNSPLSVNLIRIDSKKIDYILNLVSEAVISKSSYNQINSEMITLFY
NFNKYYDYQESFQRNFLIDLKIVFKDAGLTLEDEIESHINSLMSFKMERALKDISELT
NSFFRLLQNFKMTSGRLSRIITDLKIVFKDAGLTLEDEIESHINSLMSFKMERALKDISELT
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EGNNYLSIELEDDGIGIDPKVLTRKLLEKGTIKEDAIYSDFELINLIPARGTSRAGTILARAN
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DCKMTSGRLSRIITDLHESPLENGTIFNIKDPLTUVIQGLLVKSGSETY
DLSGRGVGLDVVKKSIEKLNGTILVESEIGLGTIFKIKLPLTLVIIQGLLVKSGSETY
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percent identity: 99.31; identified by sequence
similarity: putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="G1:268608"
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/translat
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EIFRAAHTLKGSSASLDMMELSDFTHIVEDYFDAIRDGKVNINNDLYDLLLSSLDVIK
EMLALRIDGKVYLNDISDLKSKLKQFLVIDDQTFIKRFDGNSIKNNFCLSESDLEEIR
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1168. .3762
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3769. .5169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
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identified by sequence similarity; putative"
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/db_xref="taxon:139"
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                                                                                                                                                                  98.93;
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/gene="BB0672"
5706. .6146
/gene="BB0672"
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/gene="BB0673"
/note="similar to GP:1408275 percent identity:
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/gene="BB0674"
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ISNEMIFFPRE"
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complement(6187. .6702)
/gene="BB0673"
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/db_xref="PID:q2688610"
/db_xref="FID:q2688610"
                                                                                                                                                                                          putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
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/db_xref="PID:92688603"
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/db_xref="prb:92688604"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GP:1408274 percent identity: 97.95; identified by sequence similarity; putative"
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/protein_id="AAC67022.1
/db_xref="PID:g2688605"
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/note="similar to GP:1408273 percent identity: 98.76;
identified by sequence similarity; putative"
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5181. .5666
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KLTAIDNDLSKVVETSRLVFSESEIGISEIYSRNSFEQSPGVYKFKSEILSNVLFEYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIKEKSTKYFNLYRKV"
                                                                                                                                                                                                                 /note="hypothetical protein;
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                            'db_xref="GI:2688610"
                                                                                                                                                             codon_start=1
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SOURCE
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BBU62900
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Best Local
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1 (bases 1 to 1655)

Ge, Y. and Charon, N.W.
An unexpected flah homolog is present and
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Similarity 100.0%;
21; Conservative (
                                                                                                                                                    Submitted (03-JUL-1996) Yigong of Microbiology, HSCN, Morgantown,
                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                  J. Bacteriol. 179 (2), 97144545
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia
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Borrelia burgdorferi flagellar filament outsheath protein
gene, complete cds, and chemotaxis histidine kinase (cheA)
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PID:1222502 PID:1204815 percent identity: 25.58;
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/gene="BB0676"
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frikubfeselkoliqyykbyligyinklegknysyivliqkenkelskolbuli
knyikillakkefynnentisnysyipyinklegknysyivliqkenkekkbliestfk
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IISSSKIVNSI DEKOGENI IKNIS IL NEKAYLKEKYPFILI KEKDDI IYYSKSDEI FY
YYSPSEYRVI EMEKTKFYI DKYLQRKSDSILGI FLFTLFASFTI FLAMFYKFFKASFL
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/db_xref="PID:9268869"
/db_xref="PID:92688689"
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                                                    /organism="Borrelia burgdorferi"
/strain="212"
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     /db_xref="taxon:139"
/clone="pW1 and pW2"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

esteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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                                                                                                                                                                                                                                                                            direct repeat; inverted repeat; polyubiquitin
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/gene="cheA"
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/db_xref="PlaA protein"
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/gene="flaA"
/function="putative flagellar filament outsheath protein"
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/db_xref="PID:g1575448"
/db_xref="G1:1575448"
/translation="MEILDLENEELLGVFFEEAQNLVDILEENI"
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SNEGFSFGFLLSDSRFLYSFLKNGVYYVNLSREFYDSFNNGDYNESFDVKVNLFAMSL
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/function="unknown"
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/protein_id="AAC44769.1"
/db_xref="PID:g1575446"
/db_xref="GI:1575446"
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/codon_start=3
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.K. and Pfitzner,U.M.
f a heptaubiquitin gene from tomato
ol. 104 (1), 299-300 (1994)
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/translation="MQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLI
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TGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKEST
LHLVLRLRGGMQIFVKTLTRKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGK
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                                                                                                                     GRTLADYNIQKESTLHLVLRLRGGDL"
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                                                                                                                                  ITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLV
LRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLED
                                                                                                                                                                 QDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTLTGKT
                                                                                                                                                                                                                                                                                   /product="ubiquitin"
/protein_id="CAA51679.1"
/db_xref="PID:g312160"
/db_xref="GI:312160"
                                                                                                                                                                                                                                                                                                                                                               /note="branch point"
1776. .3380
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="craigella"
/db_xref="taxon:4081"
/clone_lib="EMBL3"
/clone="1"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_type=INVERTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lycopersicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_type=DIRECT
               95.2%; Score 20; 100.0%; Pred. No.
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 Mismatches
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               DB 7;
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COMMENT
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AUTHORS
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ORGANISM
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CET25C12/c
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bin/display7db-wormacesclass-Sequence sobject-T25C12
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone T25C12. The true right end of clone F48C5 is at 13899 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence Z68107.

The end of this sequence (32937. .33045) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jesesauger.ac.uk or rwenematode.wustl.edu

2 (bases 1 to 33045)

Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,

Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,

Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,

Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,

Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,

Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,

O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,

Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,

Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,

Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,

Wilkinson-Sproat,J. and Wohldman,P., Weinstock,L.,

Wilkinson-Sproat,J. and Wohldman,P., Weinstock,L.,

Wilkinson-Sproat,J. and Wohldman,P., Weinstock,L.,
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ATGAAAAGGAAAGCTAAAAG
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Caenorhabditis elegans
Z66566
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Direct Submission
Submitted (04-NOV-1995) Louis, MO 63110, U
Submitted (04-NOV-1995) Louis, MO 63110, U
Submitted (04-NOV-1995) Louis, MO 63110, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2 Mb of contiguous nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a graphical representation of this sequence and its analysis
                               9132. .23914

/gene="lin-14"

join(9132. .9253,20428. .20645,21083.

join(9132. .9259,20428. .23088,23135. .23

22753. .22929,22980. .23088,23135. .23

23615. .23762,23807. .23914)

/gene="lin-14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z93779.
                                                                                                                                                                                                                                                                                                                                              /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                       /clone="T25C12"
note="Embryonic nuclear protein lin-14 form B2; cDNA EST
                                                                                                                                                                                                                                                                                                                   'chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                  3. .21286,22191. .222
.23350,23398. .23563,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1998
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k260all.5 comes from this

gene"

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/COGOD_STATE= PID #3380723*
// DL_TEE= PID #3380724*
// DL_TEE= PID #33
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gene

CDS

CDS

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complement(39379, 1.110. .490), complement(3923, 33045), complement(39864. 3254), complement(30262. 32773), complement(31780. 32941), complement(31780. 3344), complement(31780. 3344), complement(31780. 3142), complement(31780. 3142), complement(31780. 3142), complement(31173. 3146), complement(31173. 3122), complement(31173. 3146), complement(31173. 3122), complement(3
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JOURNAL
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TITLE
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                                                      FEATURES
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TITLE
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                           source
                                                                                                                                                                                                                               Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For furth details, see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                           Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-SEP-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Sep 19, 1998 this sequence version replaced g1:3213106.
SUBMITTED BY: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (12-JUN-1998) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Genetics Washington University St. Louis MO 63108, USA http://genome.wustl.edu/gscmailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO 63108, USA
3 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 112621)
Waterston, R.H.
                                                                    The clone sequenced to the right is I Actual start of this clone is at base actual end is at 112621 of DJ0800L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of this clone was established as part of a mapping sequencing collaboration between the NHGRI Chromosome 7 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cotton,M., Tin-Wollam,A., Sutterer,C. and Wilson,C. The sequence of Homo sapiens PAC clone DJ0800L12
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Cotton, M., Tin-Wollam, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g3638952
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AC004891
                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    This clone was derived from human PAC library RPCI-4, prepared by
                                                                                                                                                                                                                                                                                                                                                                                               SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                (http://www.genomesystems.com).
VECTOR: pCYPAC2
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/organism="Homo sapiens"
                                              Location/Qualifiers
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DJ0800L12 from 7q34-q36, complete
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                                                                                                 is DJ0676L20, 200 bp overlap.
base position 1 of DJ0800L12;
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/clone_lib="RPCI-4"
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6788. .6834
                                         complement(<21462. .>75820)
/gene="WUGSC:H_DJ0800L12.1"
complement(join(<21462. .2169
/gene="WUGSC:H_DJ0800L12.1"
/gene="WUGSC:H_DJ0800L12.1"
/note="contactin-like; similar to U87224 (PID:g1857710);</pre>
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9661. .9787
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7487. .77
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1564. .1804
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13892. .13918
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13487. .13520
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4209. .4377
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3087. .3430
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14442. .14712
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RESULT 6
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                HSU66083 73360 bp DNA PRI 29-AUG-1997 Human contig of two cosmids from LLNL X chromosome library (U83F1, U109H10), including MAGE-9 antigen (MAGE9) gene, complete cds, and three genes of unknown function.
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/gene="WUGSC:H_DJ0800L12.1"
/db_xref="GI:1113778"
36641. 36690
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mgkedfikkleksatevsfsfdvgngpveivvrspfpklodmervtaernvkqaslq
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2 Timms K.M., Bondeson,M.-L., Ansari-Lari,M.A., Lagerstedt,K.,
Nelson,D.L., Pettersson,U. and Gibbs,R.A.
Direct Submission
Submitted (05-AUG-1996) Department of Human and Molecular Genetics,
Baylor College of Medicine, One Baylor Plaza, Houston, Texas 77030,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Timms,K.M., Bondeson,M.-L., Ansari-Lari,M.A., Lagerstedt,K., Nelson,D.L., Pettersson,U. and Gibbs,R.A.
Molecular and phenotypic variation in patients with severe H
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/rpt_family="Alu"
18245. .18490
                                                                         /rpt_family="SVA"
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complement(9508.
/rpt_family="L1"
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/rpt_family-"Alu"
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complement/for:
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5773. .6002
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              rpt_family-"SVA"
                                                                                                         /rpt_family="Alu"
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misc_feature

repeat_region repeat_region

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/note="unknown function"
complement(27172. .28489)
/rpt_family="THR"
complement(28711. .28934)
/rpt_family="MSTa"
   /gene="7."
43836..44597
498ne="7."
498ne="7."
/gene="7."
/note="Region with high GC (72%) content, single coverage only; unknown function"
/note="Region: single strand coverage only."
complement(45107..45370)
/rpt_family="MSR1"
complement(48476..48744)
                                                                                                                                                                                                                                                                                                                                                                            /gene="X'"
/gene="X'"
/note="CDNA from human placental library; unknown
/note="cDNA from human placental library; unknown
function; clone 19187"
complement(join(<43030. .43261,42271. .42318,38845.
complement(join(<43030. .3361,42271. .42318,38845.
38462. .38743,37066. .>37607))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MER11A"
complement(21392. .21669)
/rpt_family="Alu"
complement(21716. .22106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=experimental complement(join(43030. .43322,42271. .42318,38845. .38977, 38462. .38743,37037. .37607))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=experimental complement(join(42979. .43311,42287. .>42318)) /gene="X'"
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complement(37037. .43323)
/gene="%"
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/rpt_family="SVA"
complement(26695...27058)
                                                                                                                                                                                                                                                                    /evidence-experimental
/oin(43465. .43023,4595. .45722,45893. .46075,46626. .4
48487. .48598.48854. .48936,50694. .52183,52914. .53011,
53142. .53230,65601. .65784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="EST from WashU-MERCK EST project; unknown function;
EST clone 115392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<42271. .42352,38845. .38977,38462. .38743,
37037. .>37607))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(26715.
/gene="Y'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Duplication of bases 178530 - 206055 from contig
formed from cosmids U69B6, U142F2, U126G1, U145C10,
112G10, 169A5 and U84H1"
/note="Region: large scale duplication."
                                                                                                                                                                                                                /note="cDNA from human placental library; unknown
function; clone Z'3-1"
                                                                                                                                                                                                                                                                                                                                              /note="cDNA from human placental library; unknown function; clone 48A8"
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13465. .68936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LA-PCR product; unknown function; clone X'-3a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⁄evidence=experimental
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lement("?".
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5, .50620
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U19974.1
                                                                                                                                                                                        XLU19974 2794 bp mRNA VRT 02-FEE Xenopus laevis poly(A) polymerase type 2 mRNA, complete U19974
                                                        Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
18; Conserv
Ballantyne,S., Bilger,A., Astrom,J., Virtanen,A. and Wickens,M.
                                                                                                                African clawed frog
                                            Kenopus
                       (bases 1 to 2794)
                                                                                                                                                                                                                                                                                                                                                                                                 85.7%; Score 18; DB 11;
larity 100.0%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 0;
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48521. .48724
/rpt_family="SVA"
49536. .49920
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/rpt_family="Alu"
61725. .61958
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/note="Region: single strand coverage."
join(<53209. .53230,65601. .>68555)
/gene="Z'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(62643. .63278)
/rpt_family="L1ME2"
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/rpt_family="Alu"
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/rpt_family="Alu"
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complement/socco
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complement/for"
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complement/socco
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/rpt_family="Alu"
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complement/<?>
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function; clone 161455-2-3"
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ement(6122'
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Best Local :
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2 (bases 1 to 40397)
Barrell, B., Rajandream, M.A. and Walsh, S.V.
Direct Submission
Submitted (22-JUN-1995) Saccharomyces cerevisiae chromosome XIII
Submitted (22-JUN-1995) Saccharomyces Centre, Hinxton Hall, Hinxton, Cambrid
                                                                                                                                                                                                                                                                                                                                                                                        g887599
Z49939.1 GI:887599
dihydrofolate reductase; END1; ERG8; MRE11; MRPL44; MTF1;
phosphomevalonate kinase; ribonuclease H; ribosomal protein L44;
phosphomevalonate kinase; ubiquitin carboxyl-terminal hydrolase.
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S.cerev
249939
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                                                           sequencing project, Sanger Centre, Hinxton Hall, Hinxton, CB10 IRQ E-mail: barrell@sanger.ac.uk
3 (bases 16981 to 22170)
Venema, J. and Tollervey, D.
RRP5 is required for formation of both 18S and 5.8S rRNA
RRB0 J. 15 (20), 5701-5714 (1996)
                                                                                                                                                                                                                                                                                    Saccharomycetaceae; Saccharomyces
1 (bases 1 to 40397)
Skelton J. and Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ballantyne, S.M
                                            97051828
                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerevisiae chromosome
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CDS over 100 codons have been analysed. CDS that are completely
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ic changes during oocyte maturation and early development(1), 64-78 (1995)
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SGGSLNESIPETATHPAFSSTPRPLVTRVVSSMPLVNQVQKPVTNTVTKMPSPVAGVK
RTSSPTNEESPKKTKTEEDENDSSNSTEVDEQNKLEPEELKEVHSEEKSSSPVPGALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="poly(A) polymerase type 2"
/protealn_id="AAC59746.1"
/db_xref="pil:9643646"
/db_xref="pil:9643646"
/translation="MLVARTCQLYPNAIASTLVHKFFLVFSKWEWPNPVLLKQPEECN
/translation="MLVARTCQLYPNAIASTLVHKFFLVFSKWEWPNPVLLKQPEECN
/LNLPVWDPRVNPSDRYHIMPIITPAYPQQNSTYNVSVTRAVWYEEFKQGLAITDEIL
LVKAEWSKLFDAPNFFGXYKHYILLASAPTEKQRLEWGLVESKIRILYGSLEKNEF
ITLAHNNPQSFFSPSENSEKEEERTMWVIGLVFKKMENSENLSVDLTYDIQSFTDTVY
RQAINSKMFFTEIKIAAMHYKKKQLHOLLPSHYLPKKKKHSVEGVKLVSLNDSSIDLS
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/db_xref="taxon:8355"
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728. .2182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA F
XIII cosmid 9959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cosmid 9959 overlapped at 5' by cosmid 8261, embl entry SC8261X, accessionno.249809 and at the 3' by cosmid 9408, embl entry SC9408,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accession no. Z48756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is given for each CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="YM9959.01, len: > 1 unknown orf, overlaps and YM8261.13"
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PNMDDYCNRNLFVIDLFSDDAYHSQEDSVTEHRGNRRLSFHSHRIEEVPKTGLGSSAG
                                                                                                                                                                                                                                                                                            /note-"YM9959.02, ERG8 gene, len: 451, CAI: 0.15, SW:ERG8_YEAST P24521, phosphomevalonate kinase; contains PS00627 GHMP kinases putative ATP-binding domain, conflict at C-terminus due to a frameshift with ERG8_YEAST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"overlap with cosmid positions 27890 to 28201" 3363. .4718
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TVKLVQKVKNWYDSHMPESLKIYTELDHANSRFMDGLSKLDRLHETHDDYSDQIFESI
                     LVTVLTTALASFFVSDLENNVDKYREVIHNLAQVAHCQAQGKIGSGFDVAAAAYGSIR
YRRFPPALISNLPDIGSATYGSKLAHLVDEEDWNITIKSNHLPSGLTLWMGDIKNGSE
                                                                                                                                                                                                                                                                                                                                                                                            3363. .4718
/gene="ERG8"
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3363. .4718
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KPSMEL I NDKSSPENNNDEET NREKDKTKAKKKSRKRNY NSRRRKKK I TEGSSAASNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Saccharomyces
/strain="AB972"
/db_xref="taxon:4932"
/chromosome="XIII"
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                                                                                                                                                                                                                                                     /db_xref="SGD:S0004833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ERG8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone-"cosmid 9959"
                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae"
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8261 orf
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CDS

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misc_feature
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KIAVEGLDENGRLIEGDTGSGIIPDEQERGSLIALEREEDSIPSRPQRRKSVLETVYE
DKLQKKSGGIIGVLHGKSAYEQIXSPWFYLMLLEALVAMLRINYEIATVTRGCEYLLN
DPDLALKLNSIFDMLLPLGGAVSIFFIGLLLDHTDTLSTLTITTTATATCVFGLLFN
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/cote="YM9959.04c", unknown, len: 223, CAI: 0.10, similar
to Sw.idx Schpt 0.36591,dihyddofolate reductase (29.4%
identity in 218 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERNDCTCQKYPEITEVRDAVATIRRSFRKITKESGADIEPPVQTSLLDDCQTLKGVLT
CLIPGAGGYDAIAVITKQDVDLRAQTANDKRFSKVQWLDVTQADWGVRKEKDPETYLD
K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="YM9959.05, unknown, len: 471, CAI: 0.17, similar to putative ubiquitin carboxyl-terminal hydrolases, eg SW:UBPX_HUMAN, P40818, probable ubiquitin carboxyl-terminal hydrolase (31.5% identity in 352 aa overlap); contains PS00973 Ubiquitin carboxyl-terminal hydrolases family 2 signature 2"
                                                                                                                                                                                                                                                                                                              LLTCAWKINQNLAGYSQODAHEFWQFIINQIHQSYVLDLPNAKEVSRANNKQCECIVH
TVFEGSLESSIVCPGCONNSKTTIDPFLDLSLDIKDKKKLYECLDSFHKKEQLKODNY
HCGECNSTODAIKQLGIHKLPSYLVLQLKRFEHLLNGSNRKLDDFIEFTYLNMKNYC
STKEKDKHSENGKVPDIIYELIGIVSHKGTVNEGHYIAFCKISGGQWFKFNDSMYSSI
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membrane protein"
/note="YM9959.06c, MRE11 gene, len: 692, CAI: 0.14, SW:MR11_YEAST, P32829, required for repair and meiotic recombination, conflict, this sequence is longer due to
                                                                                       complement(9622. .11700)
/gene="mrel1"
                                                                                                                                                                                            /note="PS00973 Ubiquitin carboxyl-terminal hydrolases
family 2 signature 2"
complement(9622. .11700)
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                                                                                                                                           /gene="MRE11"
/db_xref="SGD:S0004837"
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ORGANISM
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KEYWORDS
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Best Local S
Matches 19
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TITLE
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  This sequence was generated from part of bacterial clone contigs of
                                  feature key.
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Sg

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30511 AGGAAAAGGAAAGGTAAAAGT 30531
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| ||||||||||| |||||||
requests: clonerequest(sanger.ac.uk
On May 4, 1999 this sequence version replaced gi:4678569.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL
This sequence is the entire insert of clone 753D10. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-JUN-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSJ753D10 97912 bp DNA PRI 10-JUN-1999 HSJ753D10 On chromosome 20, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL049651.2 GI:4741619
HTG; CpG Island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matthews, L.
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HTNTAFLPEOGTLPDFLDMVIWGHEHECIPNLVHNPIKNFDVLDGGSVYATSLCEAEAQ
PKYVFILDIKYGEAPKMTPIPLETIRTFKMKSISLQDVPHLRPHDKDATSKYLIEQVE
EMIRDANEETROKLANDGEGDMVAELPKPLIRLRVDYSAPSNTQSPIDYQVENPRRFS
EMIRDANEETROKLANDGEGDMVAELPKPLIRLRVDYSAPSNTQSPIDYQVENPRRFS
NRFVGRVANGNNVVQFYKKRSPVTRSKKSGINGTSISDRDVEKLFSESGGELEVQTLV
NDLLNKMQLSLLPEVGLNEAVKKFVDKDEKTALKEFISHEISNEVGILSTNEEFLRTD
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complement(join(12007. .12245,12393. .12450))
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HVDNESRITHISQAESSKPTSKPKRVRTATKKKIPAFSDSTVISDAENELGDNNDAQD
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NNNVDMYVQSGDLFHVNKPSKKSLYQVLKTLRLCCMGDKPCELELLSDPSQVFHYDEF
TNVNYEDPNFNISIPVFGISGNHDDASGDSLLCPMDILHATGLINHFGKVIESDKIKV
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/db_xref="PID:g887605"
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/db_xref="SGD:S0004837"
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                     /note="8 copies 4 mer gtgt 100% conserved" 26711. .26744
                                                          /note="MER5A repeat: matches 1. .189 of consensus" 26711 . .26742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9082. 9392
/note-"Alusx repeat: matches 1. .312 of consensus"
9393. 9575
/note-"MLT1A1 repeat: matches 154. .362 of consensus"
9905. 10360
/note-"LTRA3 repeat: matches 1. .513 of consensus"
10452. .10849
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/note="HAL1 repeat: matches 274. .810 of consensus"
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/note="THE1C repeat: matches 1..371 of consensus" 12305..12549
/note="TLMC3 repeat: matches 7491..7739 of consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organ1sm="Homo sapiens"
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/chromosome="20"
                                                                                                                                                                                                                                                   15978.
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'note="L1MD repeat: matches 4. .350 of consensus"
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                                                                                                             e="L2 repeat: matches 2646, .2695 of 0. .23287 e="2 copies 39 mer 99% conserved"
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 copies 2 mer gt 100% conserved"
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                                                                                                                                                                                                                                                                                                      .301 of consensus"
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                                                 /note="7 copies 30 mer 72% conserved"
47579. .47779
/note="67 copies 3 mer tac 71% conser:
47582. .47776
/note="5 copies 39 mer 79% conserved"
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/note="MER53 r
48135. .48162
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/note="Alusg r
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/note="MER66B repeat:
45120. .45317
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/note="10 copies 30 mer 77% conserved"

38355. .38410

/note="14 copies 4 mer atat 79% conserved"
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/note="L2 repeat: matches 2628.
29111. .29160
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45549. .45879
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/note="27 copies 2 mer at 80% conserved"
39756. .40043
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/note="LTR16C repeat:
30535. .30676
                                                                                                                               /note="MIR repeat: matches 19. .262 of
47577. .47786
/note="7 copies 30 mer 72% conserved"
                                                                                                                                                                                        47319. .47569
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43323. .43475
/note="L2 repeat: matches 2246.
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43031. .43320
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42866. .42992
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36129. .36418
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34850. .35115
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                                                                                                                                                                                                                       note="L1MEc repeat: matches 549. .967 of consensus" 16397. .46572
                                                                                                                                                                                                                                                                 'note="L1MEc repeat: matches 1073. .1400 of consensus"
15957. .46367
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9. .38352
e="157 copies 2 mer ta 76% conserved"
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                                                                                                                                                                   Cambridgeshire, CBIO ISA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 12, 1999 this sequence version replaced gi:5050930.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.ocil, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJII14Al Contig_ID: 01302
acc=AL035684 Length: 17033 bp Unfinished: dJII14Al Contig_ID:
02484 acc=AL035684 Length: 17033 bp Unfinished: dJII14Al
Contig_ID: 01371 acc=AL035684 Length: 1223 bp.
* NOTE: This is a 'working draft' sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atgaaaaggaaagctaaaagt 21
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1 (bases 1 to 153361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laird, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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/note="LTR26 repeat: matches 308. .461 of consensus"

52967. .53373

/note="MER48 repeat: matches 1. .398 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER49 repeat: matches 448. .736 of consensus"
54325. .54540
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                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
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54541. .54927
                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jun 11, 1999 this sequence version replaced gi:4995276.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
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thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 111641 bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="20"
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90.5%;
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Pred. No. 1.9e+02;
Pred. No. 1.9e+02;
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Pred. No. 1.8e+02;
0; Mismatches 2
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Direct Submission

Submitted (23-MAR-1999) MIPS, at the Max-Planck-Institut fuer submitted (23-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 viewed at: http://websyr.mips.blochem.mpg.de/proj/thal/.
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Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 99856)
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/product="putative protein"
/product="cab39774.1"
/protein_id="Cab39774.1"
/protein_id="Cab39774.1"
/db_xref="piD:e4420109"
/db_xref="piD:e44538950"
/db_xref="piD:e44538950"
/db_xref="piD:e44538950"
/translation="MKMKLGYSLPVMCMILFCYILCCSLLMSHCHGVVEAAKALKSNE
/LEOKLELINKHTVKIIKCTNGERYGCVDFYKOPGLDHSLMKNHTEHHKWRLMSYP
EGSKIKKOTHINKTFGHFWKNGVGRPIGTVFILLVSKEALLKNKSFDODNSNOSSWS
KIYKPTSSNGGHHFAVVRTTKGKPRRYNGVAMNINSFNPFMEFSAGRMNFOIGNE
FVQVGWTVRGHGCYNPLCPVGSGIILVSHEVTPGLLTKHNDFELSIIKDKIYGHWHL
FVGNSSSTWKEIGFWFTHREKESFGTGVEWGGEVYSPASTSPMGNSHFPKGSPKIDS
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2972. .
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thaliana, AJ011845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVRLITTWDENYGLDMVVKNTERFSNSCYKVKDAQSRFGQM"
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                                                                   1658. .4908
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    /gene="F24G24.10"
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                                                                                                                                   14529. .15088
/gene="F24G24.40"
complement(14529.
/gene="F24G24.40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTSILSAVSKLRGCVNQIENKNPSGASEEDILNQAKMLLTQYEK
YKRGEKEDHYWPILKGIEKEADDNKTPBAEFGGEGRDVTSSSSESSINTESSPSPGMNS
IDLMNDSEDANESLSSRPMGLKKAKRRQOSEEQFKOLLEGNDKLIKATTKGTSERREI
ORQKIEVARMKEENKILFADLNSISDPSSRAYVENERKRILEKRAGTNQHEEDGEGSO
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/gene="F24624.30"

/oin(11823. .11915,12019. .12747)

/gene="F24624.30"

/codon_start=1
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Allewkspdsdnsnpgswskyykpassiddheavvpttkgtbsyngasmintety
Svcpmofsasrmhfolgneffoygmidkingnmllmgtsweevgfwbssrfkessgt
Mvemggevyspsppnppmgnshypkgspkvdsyvrlittvdenyntdktvknterysd
                     /note="strong similarity to zinc-finger protein R2931,
Oryza sativa, PIR3:JE0116"
                                                                 complement(join(14529. .14816,14888. .15088))
/gene="F24G24.40"
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9555. .10284
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/gene="F24G24.20"
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/protein_1d="CAB39775.1"
/db_xref="piD:e1420110"
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thaliana, AJ011845"
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join(8685. .8915,9402. .9554,10285. .10641)
/gene="F24G24.20"
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5028. .5488
/gene="F24G24.10"
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12019. .12747
/gene="F24G24.30"
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/gene="F24G24.30"
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/number=1
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/db_xref="PID:e1420111...
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/gene="F24G24.20"
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/db_xref="GI: 4538951"
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/codon_start=1
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Saccharomycur-1
1 (bases 1 to 12388)
1 (bases 1 to 12388)
Wolfe,K.H. and Lohan,A.J.E.
Sequence around the centromere of Saccharomyces cerevisiae
Sequence around TI: similarity of CEN2 to CEN4
                                                                                                                            Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                     centromere 2; hexaprenyl pyrophosphate synthetase;
histone H2B; trehalase.
                                                                                                                                                                                                                                                                                                                                          SCHISTRE 12388 bp DNA
S.cerevisiae genes for histone H2A and
hexagrenyl pyrophosphate synthetase.
                                                                                                                                                                                                                                                                         Z26494.1 GI:403311
                                                                                                                                                                                                      baker's yeast.
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16099 16606
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17671..18081,18156..18332))
179ene="F24624.60"

/EC_number="2.7.1.4"

/note="strong similarity to fructokinase, Lycopersicon esculentum, gb:062329; Contains pfkB family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MMKHLLSIFFIGALLLGNIKTSEGSLSSALETTPGSLLSDLWLD RFDDPFKILERIPLGLERDTSVALSPARVDWKETAEGHEIMLDIPGLKKDEVKIEVEE NGVLRVSGERKREEEKKGDQWHRVERSYGKFWRQFKLPDNVDMESVKAKLENGVLTIN LTKLSPEKVKGPRVVNIAAEEDQTAKISSSESKEL" complement(17048...17182)
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VALQKDAASATTASGAPLCDICQERKGYFFCLEDRAMLCNDCDEAIHTCNSHQRFLLS
GVQVSDQSLTENSECSTSFSSETYQIQSKVSLNSQYSSEETEAGNSGEIVHKNPSVIL
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/gene="F24G24.40"
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/protein_id="CAB39777.1"
/db_xref="PID:e1420112"
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/gene="F24G24.60"
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/db_xref="GI: 4538954"
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/gene="F24G24.50"
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94.7%;
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Pred. No. 2.
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.18332))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVQLSVPLRETLRIVRDGAESKLTLSKFPSNLDEPSNETKQELYPTLSKILGTRDDET
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MHEYDFPRILSTFKGLIEDGYKSYSELEWLPLLFTFLHFINNKEELALRTNASHAIMK
FIDFINEKPNLNEASKSISMLKDILLPNIRIGLRDSLEEVQSEYYSYLSYMYKNTKYF
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CIQLLALLVQVLDEDEVIAEGEKILLPLYGYLETYYSRAVDEEQEELRTLSNECLKIL
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EHYVFSDDERYRNIGNETQIAIGGLAQHMSWNQYKALLRRYISMLKTKPNQMKQAVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone-"cosmid alpha 308.2"
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       'db_xref="SWISS-PROT:P02294"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="COO1 (YBR0109)"
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11534. .>12388
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/gene="YBL0105"
complement(5878. .6192)
/gene="YBL0105"
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complement(7666. .10008)
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chromosome IV (accession number X65925)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA81269.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="homolog of unidentified ORFs in corynebacterium (LU7603) and Streptomyces (M29297)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="YBR0106"
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                                                                                                                           note="overlap with accession J05547"
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                                                                                                                                                               (YBR0109)"
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AL Submitted (30 Aug-1994) Data collected by MIPS on behalf of the European yeast chromosome II sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org

CE 5 (bases 1 to 14999)

RS Feldmann, H., Algle, M., Aljinovic, G., Andre, B., Baclet, M.C., Barthe, C., Baur, A., Becam, A.M., Biteau, N., Boles, E., Brandt, T., Contreras, R., Crouzet, M., Epsuch, C., Demolis, N., Delaveau, T., Dolygnon, F., Domdey, H., Desterhus, S., Dubois, E., Dujon, B., El Bakkoury, M., Entian, K.D., Feuermann, M., Fiers, W., Fobo, G.M., Fritz, C., Gassenhuber, H., Glansdorff, N., Goffeau, A., Grivell, L.A., de Haan, M., Hein, C., Herbert, C.J., Hollenberg, C.P., Holmstrom, K., Jacq, C., Jacquet, M., Jauniaux, J.C., Jonniaux, J.L., Kallesoe, T., Kirchrath, L., Roetter, P., Korol, S., Liebl, S., Loghe, M., Mass, F., Obermaler, B., Perea, J., Mat, M.J., Meller, S., Pohl, T.M., Pohl, T.M., Potier, S., Proft, M., Purnelle, B., Ramezani Rad, M., Rieger, M., Rose, M., Schaaff-Gerstenschlaeger, I., Smits, P.H.M., Souclet, J.L., Steensma, H.Y., Stucka, R., Verter, J., Vassarotti, A., Verter, J., Vascarotti, A., Verter, J., Vascarotti, A., Verter, J., Vascarotti, A., Verter, J., Vascarotti, A., Verter, J., Zayulski, M., Zimmermann, F.K., Mewes, H.W. and Kleine, K. Complete DNA sequence of yeast chromosome II
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1 (bases 1 to 2817)
Delaveau, T., Jacq,C. and Perea, J.
Unpublished
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.cerevisiae chromosome
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Lohan, A.J.E. and Wolfe, K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 14999)
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/db_xref="gip:9403318"
/db_xref="gip:403318"
/db_xref="gip:403318"
/db_xref="gip:3015"
/db_xref="gip:30
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94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.4;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 11-MAR-1998
ORF YBL004w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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FEATURES
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On Mar 9,
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                                                                                                                                                                                                                                                                                                                                                                                                   PGYALHPSRNSYGYIIYLPSLKKTYDJTNYVIIQGKESRLDQFNYDALIFDEDLNRII
ASYQSTIASNELQQSNDLNIESDHDFQSDIELYEQGPRNYLSKAVSFTDSTPFSTHTE
DSKRYGKTNIRAPREVDPNIESSNILPSKRKSTPQISDIESTDSGGHRHLDVPLLAP
MSQSNTHESSYASKSKDFRHSDSYSDNETNHTNVPISSTGGTNNKTVPQISEQETEKR
IIHRSPSIDTSSESNILHHVPIKTSDTCPKENTESSIIADLUPEPPFELSD
SFKELPPINSRQTNSSLGGIGDSNAVTTINKKRSLEDNETEIKVSRDTWTKNMKSL
EPPRSKKRIHLIAAVKAVKSIKPIRTTLRYDEAITYNKDIKEKEKYIEAYHKEVNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDELPGHLILDSGASRTLIRSAHHIHSASSNPDINVVDAQKRNIPINAIGDLQFHFQD
NTKTSIKULHTRUIAYDLISLKELAAVDITACETKULERSDGYVLAPIVKYGDFYWV
SKKILLPSNISUPTINUVHTSRSTRKYVPYFHIRMLAHANAQTITRYSLKANTITYSHW
SDVDWSSAIDYQCPDCLIGKSTKHRHIKGSRLKYQNSYEPFQYLHTDIFGPVHNLPKS
APSYFISFTDETTKFRWYYPLHDRREDSILDVFTTILAFIKNGFQASVLVIQWDRGSE
YTNRTLHKFLEKNGITPCYTTTADSRAHGVAERLNRTLLDCRTQLQCSGLPHNLMFS
AIEFSTIVRNSLASPKSKKSARQHAGLAGLDISTLLPFGQPVIVNDHNPNSKIHPRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNGSTPADAFEAEVTNILDRLNNNGIPINNKVACQFIMRGLSGEYKFLPYARHRCIHM
TVADLFSDIHSMYEEQQESKRNKSTYRRSPSDEKKDSRTYTNTTKPKSITRNSQKPNN
SQSRTARAHNVSTFNNSPGPDNDLIRGSTTEPIQLKNTHDLHLGQELTESTVNHTNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVSTQANSQQPTTPPSSAVPENHHHASPQAAQVPLPQNGPYPQQRMMNTQQANISGWP
VYGHPSLMPYPPYQMSPMYAPPGAQSQFTQYPQTVGTHLNTPSPESGNSFPDSSSAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYGHPSLMPYPPYQMSPMYAPPGAQSQFTQYPQYVGTHLINTPSPESGNSFPDSSSAKS
NMTSTNQHVRPPPILTSPNDFLNWVKIYIKFLQNSNLGDIIPTATRKAVRQMTDDELT
FLCHTFQLFAPSQFLPPWVKDILSVDYTDIMKILSKSINKMQSDTQEVNDITTLATLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q12266"
/translation="MESQQLSQHSPIFHGSACASVTSKEVQTTQDPLDISASKTEECE
KVSTQANSQQPTTPPSSAVPENHHHASPQAAQVPLPQNGPYPQQRMMNTQQANISGWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVADLFSDIHSMYEEQQESKRNKSTYRRSPSDEKKDSRTYTNTTKPKSITRNSQKPNN
SQSRTARAHNVSTYNNSPGPDNDLIRGSTTEPIQLKNTHDLHLRPGTY"
                                                                                                                                                                   DLLYYINTLAQHILFPSKQVLDMTYELIQFIWNTRDKQLIWHKSKPVKPTNKLVVISE
ASYGNQPYYKSQIGNIYLLNGKVIGGKSTKASLTCTSTTEAEIHAISESVPLLNNLSY
                                                                                                                                                                                                                                                                     KSLYGLKQSGANWYETIKSYLIKQCGMEEVRGWSCVFKNSQVTICLFVDDMVLFSKNL
NSNKRIIDKLKMQYDTKIINLGESDEEIQYDILGLEIKYQRGKYMKLGMENSLTEKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLCHTFQLFAPSQFLPPWVKDILSVDYTDIMKILSKSINKMQSDTQEVNDITTLATLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMTSTNQHVRPPPILTSPNDFLNWVKIYIKFLQNSNLGDIIPTATRKAVRQMTDDEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA84820.
/db_xref="PID:g535981"
/db_xref="GI:535981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999 this sequence version replaced gi:535979.
Location/Qualifiers
/note="5
                                                                                                 IETKKNIADVMTKPLPIKTFKLLTNKWIH"
                                                                                                                             LIQELDKKPITKGLLTDSKSTISIIISNNEEKFRNRFFGTKAMRLRDEVSGNHLHVC)
                                                                                                                                                                                                                               KLNVPLNPKGRKLSAPGQPGLYIDQQELELEEDDYKMKVHEMQKLIGLASYVGYKFRF
                                                                                                                                                                                                                                                                                                                                       NTVHHYALMTSLSLALDNNYHITQLDISSAYLYADIKEELYIRPPPHLGMNDKLIRLK
                                                                                                                                                                                                                                                                                                                                                                   KMKTWDTDKYYDRKEIDPKRVINSMFIFNRKRDGTHKARFVARGDIQHPDTYDSGMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MESQQLSQHSPIFHGSACASVTSKEVQTTQDPLDISASKTEECE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q12490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TY1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNGSTPADAFEAEVTNILDRLNNNGIPINNKVACQFIMRGLSGEYKFLPYARHRCI
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/db_xref="PID:g535980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene='
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nt direct repeat TGGTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nt direct repeat GGAAT; Tyl target sequence"
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BASE COUNT ORIGIN

5064

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Query Match Best Local Matches

18; Conservative Similarity

0;

Score 17.4; DB 7; Pred. No. 3.8e+02; 0; Mismatches 1

DB 7;

Length 14999; Indels

0;

Gaps

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82.9%; 94.7%;

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,note="3' del+- -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLVFVIKELMATLKRGSQIHVLSYTVHYILKSMHGVLKHSDLDTSSSMIVKIIMENIF
GFAGEEKDSENYHTKVKEIKSNKSYDAGEILASNISLTEFGTLLSPVKALLMVRINLR
NQNKLSELLRRYLLGLNHNSDSESESILKFCHQLFQESEMSNSPQIPKKKVKDQVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDDERYRNIGNETQIAIGGLAQHMSWNQYKALLRRYISMLKTKPNQMKQAVQLIVQLS
VPLRETLRIVRDGAESKLTLSKFPSNLDEPSNFIKQELYPTLSKILGTRDDETIIERM
PIAEALVNIVLGLTNDDITNFLPSILTNICQVLRSKSEELRDAVRVTLGKISIILGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELYTTISSLFKTFDERNLRVSLTELFIELGRKVPELESISKLVADLNSYSSSRMHEYD
FPRILSTFKGLIEDGYKSYSELEWLPLLFTFLHFINNKEELALRTNASHAIMKFIDFI
NEKPNLNEASKSISMLKDILLPNIRIGLRDSLEEVQSEYVSVLSYMVKNTKYFTDFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRISHESDENLQQPSSLLRLFLYWAHNPSLYQFLYYDEFATATALMDTISNQHVKEAV
IGPIIEAADSIIRNPVNDDHYVDLYTLICTSCLKILPSLYVKLSDSNSISTFLNLLVS
ITEMGFIQDDHVRSRLISSLISILKGKLKKLQENDTQKILKILKLIVFNYNCSWSDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTLPNVYTKDEALVWKLVLSFIKLPDENQNLDYYQPLLEDGANKVLWDSSVVRLRDTI
DTFSHIWSKYSTQNTSIISTTIERRGNTTYPILIRNQALKVMLSIPQVAENHFVDIAP
FVYNDFKTYKDEEDMENERVITGSWTEVDRNVFLKTLSKFKNIKNVYSATELHDHLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6556. .6560
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NGYYQRRNKRKRA"
2807 c 263
                                                                                                                                                                                                ILSDTSVGSEHQWDLVYSALNTFSSYMEATESVYKHGFKDIWDGIITCLLYPHSWVRQ
SAANLVHQLIANKDKLEISLTNLEIQTIATRILHQLGAPSIPENLANVSIKTLVNISI
                                                                                                                                                                                                                                                                            GRQSVMELINLIITKANPALLSKLSSSFFLALVNVSFNDDAPRCREMASVLISTMLPK
LENKDLEIVEKYIAAWLKQVDNASFLNLGLRTYKVYLKSIGFEHTIELDELAIKRIRY
                                                                                                                                                                                                                                                                                                                                                                                        DSLLSENEGVVISTLRILITLIRLDFSDESSEIFKNCARKVLNIIKVSPSTSSELCOM
GLKFLSAFIRHTDSTLKDTALSYVLGRVLPDLNEPSRQGLAFNFLKALVSKHIMLPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEDEKVVMPYVLRIFFGRAQVPPTSGQKRSRKIAVISVLPNFKKPYINDFLSLASERL
DYNYFFGNSHQINSSKATLKTIRRMTGFVNIVNSTLSVLRTNFPLHTNSVLQPLIYSI
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PSESLKGLMSHYPSLLLSLTDNFMLPDGKIRYETLELMKTLMILQGMQVPDLLSSCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHFLASFDQWKEINLSAKFTEFAAEIEHDVQTLPQILYHDKKIFNSLVSFINFHDEFS
LQPLLDLLAQFCHDLGPDFLKFYEEAIKTLINLLDAAIEFESSNVFEWGFNCLAYIFK
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7239. .14720
                                                                            VSDFTKIYTAVKQTVLERRKERRSKRAILAVNAPQISADKKLRKHARSREKRKHEKDE
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ALLVQVLDEDEVIAEGEKILLPLYGYLETYYSRAVDEEQEELRTLSNECLKILEDKLQ
                                                                                                                                                                                                                                                                                                                                                            YDIADTTREIMVTNHSKEIRDVSRSVYYQFLMEYDQSKGRLEKQFKFMVDNLQYPTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDFFLVNLESKSYTINSNSLLLNSTLQKFALDLLRNVITRHRSFLTVSHLEGFIPFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAILLYNGDEEADFFTNVNHIQLHRRQRAIKRLGEHAHQLKDNSISHYLIPMIEHYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMAYYVLDTESTEEVHLRKMASNLRQQGLKCLSSVFEFVGNTFDWSTSMEDIYAVVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLGSRNTDVQKLALDALLAYKNPTLNKYRDNLKNLLDDTLFKDE1TTFLTENGSQS1K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEEIPLTLQNARDLTIRIKNVGAEFGKTKTDKLVSSFFLKYLFGLLTVRFSPVWTGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNFPEEFILSIRDFFVTAEINDSNDLFEIYWRAIIFKYSKLQNTEIIIPLLERIFSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K I TILLER IMSQSENCASLSQDKVAFLFALFIRNSDVKTLTLFHQKLFNYALTNISDC
FLEFFQFALRLSYERVFSFNGLKFLQLFLKKNWQSQGKKIALFFLEVDDKPELQKVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIWMNISKYASIESLLILFTESMTSTQETLHSKAKAIMSVLLHEALTKSSPERSVSLLS
DIWMNISKYASIESLLFVYEVMYQDFNDSLDATNIDRILKVLTTIVFSESGRKIPDWN
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/note="ORF YBL004w"
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gene="TY1A"
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KEYWORDS
SOURCE
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T9A4
                                                                                                            FEATURES
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                                                                                       source
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2 (bases 1 to 83922)
Zidanic, M., McQuerry, Y. and SI
The sequence of A. thaliana Ti
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, Washu, to pick the best candidates for sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not be the entire insert of this clone It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (01-OCT-1998) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 83922) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis
                                                                                                                                                                                                                                           position
                                                                                                                                                                                                                                                                   The 3' clone is T17F16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neighboring submissions.
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                                                                                                                                 program
                                                                                                                          sequences below are predicted from computer analysis, using ogram Genefinder(P. Green and L. Hillier, ms in preparation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thaliana Genome
                                                                                                                                                                                                                                           lone is T17F16. Actual start of this clone is 1 of T9A4; actual end is at 83992 of T9A4.
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Department of Genetics, Washington University,
St. Louis, MO 63108, USA
e-mail: rwilson@watson.wustl.edu
                  /organism="Arabidopsis
/cultivar="Columbia"
/db_xref="taxon:3702"
/clone="T9A4"
                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                      NEIGHBORING COSMID INFORMATION:
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DFVEVYFQSLDEDESVSKQVLVSQLMIKRKFMFPT"
complement(5712...9371)
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FLITMIGLIVSQLSFLTICIFLISITERQNLQRDPINFNVLNITLEVIRYFCNGSAYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(5712.
9046. .9371))
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                                                                                                                                                                                                                                                                                                         /note="contains similarity to the pfkB carbohydrate kinases (Pfam: PF00294, E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="G1:3695408"
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R$V$QGKRFSS$Y$AavT$SGESEKAKKAEESLRTVMYL$CWGPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(26302. .26574)
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29759. .2984.3*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGFTTGYSCERRVDISDGGCKDASYGFAGRWSPMGKFVLIIVMFYGRFKQFTAKSGRA
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                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar
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n (GB:X59882)"
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.2191,2298. .2481,2533.
.3161)
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5653 GAAAAGGAATGCTAAAAGT 5671
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                     3 gaaaaggaaagctaaaagt 21
                                                                                                  . Similarity
18; Conserv
                                                                                                     Conservative
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complement(join(34194. .34922,35026. .35118))
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RTTKCTRSYNGASMNINTFTFSVGPMQFSASRHHFQIGNEFIQVGWIDKINGNWWLLM
GTSWEEVGFWPSSRFKESSGTMVEWGGEVYSPSPPNPPMGNSHYPKGSPKVDSYVRLI
TTVDENYNTDKTVKNTERYSDSCYKVRDATETFWSHVGHLIIYGGPGCK"
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complement(30255. .30842)
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/complement(30255. .30842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="T9A4.9"
complement()oin(36300. .36656,37387. .37539,38026. .38214,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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GVQVSDQSLTENSECSTSFSSETYQIQSKVSLNSQYSSEETEAGNSGEIVHKNPSVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains similarity to Arabidopsis thaliana salt-tolerance protein (GB:X95572) and CONSTANS-like 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="T9A4.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MMKHLLSIFFIGALLLGNIKTSEGSLSSALETTPGSLLSDLWLD
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NGVLRVSGERKREEEKKGDQWHRVERSYGKFWRQFKLPDNVDMESVKAKLENGVLTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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/db_xref="PID:g3695409"
/db_xref="GI:3695409"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTKLSPEKVKGPRVVNIAAEEDQTAKISSSESKEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains similarity to heat shock hsp20 proteins
(Pfam: PF00011, E=1.2e-46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                           82.9%;
94.7%;
                                                                                                     0
                                                                                                  Pred. No. 2.9
0; Mismatches
                                                                                                                                                       Score 17.4;
                                                                                                                           4; DB 8;
2.9e+02;
                                                                                                                                                    Length 83922;
                                                                                                  0;
                                                                                                  Gaps
                                                                                                  0
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B 8

Search completed: August 18, 1999, 17:17:01 Job time: 3467 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic nucleic search, using sw model

Run on: August 18, 1999, 17:18:23; Search time 148.09 Seconds (without alignments) 35.479 Million cell updates/sec

Title: Perfect score: Sequence: US-09-004-395-3 21 1 atgaaaaggaaagctaaaagt 21

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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RESULT 3
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Continuation (9 of 17) of V21209 from base 800001 (Methanococcus jannaschii circular WP Sequence split into 17 fragments LOCUS V21209 Accession V21209
WP V21209_00 1 10000
WP V21209_01 10000 210000
WP V21209_02 200001 310000
WP V21209_03 300001 410000
WP V21209_05 500001 510000
WP V21209_05 500001 710000
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WP V21209_08 800001 910000

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Query Match Best Local S Matches 21	RESULT 2  X20248_02/c  CONTINUATION (3 of 10) WP Sequence split into WP ST20248_01 WP X20248_01 WP X20248_02 WP X20248_03 WP X20248_04 WP X20248_05 WP X20248_06 WP X20248_08 WP X20248_08 WP X20248_08	Query Match Best Local: Matches 2 Matches 1  Qy 1 atg. Db 105140 ATG.	RESULT 1  X20248_01/c  X20248_01/c  Continuation (2 of 10)  WP Sequence split into WP Fragment Name WP X20248_01 WP X20248_02 WP X20248_03 WP X20248_03 WP X20248_05 WP X20248_05 WP X20248_06 WP X20248_07 WP X20248_07 WP X20248_07 WP X20248_08 WP X20248_09 WP X20248_09 WP X20248_09 WP X20248_09	45 15.4	
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Score 21; D Pred. No. 1. ; Mismatches	om base 200001 Locus x20248 End 320000 110000 310000 410000 410000 610000 610000 710000 810000 910715	re 21; d. No. ismatc	from base 100001 its LOCUS X20248 110000 210000 310000 410000 510000 610000 610000 710000 810000 910715	V35134  ALIGNMENTS	133
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Length 110000; Indels 0;	lia burgdorferi lon x20248	ngth 110000; Indels 0;	lia burgdorferi lon X20248	Microbial	Microbial
Gaps 0		Gaps 0;			l L-alpha-
0;	polynucleot1d	÷	polynucleotid		

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PT New isolated cancer associated nucleic acids and polypeptides - PT isolated using sera from cancer patients, used to develop products PT for the diagnosis, monitoring or treatment of cancers

CC The invention relates to a method for diagnosing a disorder characterised CC by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a CC biological sample isolated from a subject with an agent that specifically conduct complexed with an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the contaction between the agent and the NAM or the expression product as a CC determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. CC The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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15-JUL-1998; U14679.
22-JUN-1998; US-102322.
17-JUL-1997; US-896164.
10-OCT-1997; US-061599.
10-OCT-1997; US-061765.
11-OCT-1997; US-048705.
11-OCT-1997; GB-021697.
(LUDW-) LUDWIG INST CANCER RES.
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X40071;
02-JUL-1999
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 1242
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                                                                                                             lung cancer.
Sequence 2569
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              tgaaaaggaaagctaaaagt
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    colon cancer; gastric cancer; renal cancer; lung cancer;
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VRESULT 5

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N81546
ID NE AC NE DT 0.0
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CC The invention relates to nucleic acid sequences (V84411 to V84633) composition for the composition with the ATCC under deposit numbers ATCC gene sequences are deposited with the ATCC under deposit numbers ATCC (C 29799, 97974, 97975, 97976, 97977, 209087, 209088, 20909, 209010, CC 209011, 209080, 209081, 209082, 209082, 209010, CC 209011, 209080, 209081, 209082, 209083, 209085, 209511 Host CC ells comprising recombinant vectors containing the nucleic acid content for preventing, treating or ameliorating the secreted consecution of the secreted proteins. The polynucleotide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides, based on which tissues they are most highly expressed in, and include developing creating the presence of materiant of the management of the polynucleotides.
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                                                                                                       RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                      products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, tumours, leukemias, diseases of the immune system, autoimmune diseases, thepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The present sequence represents a gene encoding a human secreted protein (see descriptor line for gene number and clone identification).

Sequence 1288 BP; 356 A; 264 C; 295 G; 370 T;
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05-SEP-1997;
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05-SEP-1997;
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06-JUN-1997;
05-SEP-1997;
05-SEP-1997;
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Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress G
Ean P, Feng P, Ferrie AM, Fischer CL, Florence C,
Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,
Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
WPI; 99-059865/05.
P-PSDB; W88648, W88934
04-DEC-1990 (first entry)
Bio A, Bio B and Bio D-encoding fragment of B.sphaericus IFO 3525.
                                             N81546 standard; DNA; 4382 BP
N81546;
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US-057654.
US-057666.
US-057763.
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Pred. No. 1e
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Bacillus sphaericus.
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/*tag= g
/label=possible:
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/note-"Bio B"
3156. .3158
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510. .512
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2566. .2568
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1574. .1576
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1431. .1433
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2599. .2601
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2530. .2532
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/label=possible
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/note="Bio D"
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/function-possible termination site
/note-"palindromic regions - 4317-4333
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2509. .3159
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Matches 18
                                                                                                                                      W09312136-A.
24-JUN-1993.
09-DEC-1992; U10930.
11-DEC-1991; US-805093.
27-MAY-1992; US-888839.
30-CCT-1992; US-971094.
(UTJE-) UNIV JEFFERSON THOMAS.
Canaani E, Croce CM;
WPI; 93-214090/26.
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04-MAY-1988.
28-SEP-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A second clone was isolated which contained bio C. The insert present in the plasmid of insert from pTG1400 were cloned together in plasmid (pTG1440) which complements biotin a process of the process of the plasmid (pTG1440) which complements biotin a process of the process o
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DNA was isolated from B.sphaericus IFO 3525, cut with HindIII and the fragments sub-cloned into pBR322. The recombinant plasmids were used to transform E.coli bio- mutants. Plasmid pTG1400 was present in one clone (E.coli C600; CNCM I-608) which showed complementation for bio A and bio D. The plasmid contains a 4.3kb insert which includes 4 long open reading frames (LORFs) as described in the Features Table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 88-121306/18.
p-PSDB; P81188, P81189, p81190, p81191.
New DNA sequences encoding enzymes involved in biotin biosynthesis isolated from Bacillus sphaericus, and transformants useful in fermentative biotin production.
  Claim
This :
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Gloekler R, Speck D, Lemoine
WPI; 88-121306/18.
P-PSDB; P81188, P81189, P8119
                                                                                            P-PSDB; R38470.
Detection and treatment
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18-MAY-1987;
                                                   chromosome 11
                                                                    Detection and treatment of acute leukaemia(s) derived from oligo:nucleotide sequences within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALL-1 gene cDNA.

ACUTE lymphoblastic leukemia gene; ALL-1; chromosome 11; treatment; translocation breakpoint mapping; chromosomal abnormality; diagnosis; human; acute lymphocytic; myelomonocytic; monocytic; myelogenous;
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Q43526;
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85.78;
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English.
ne cDNA clone
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No. 1.3e+02;
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                                                                 using prods.the ALL-1 gene
acute lymphoblastic
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Non-control of the control of the control of the control of types of fluorescence in situ hybridisation (FISH). The probe detects fundance 1420 Bp; 451 A; 323 C; 348 G; 298 T;
    Q 23477. Q 253477. Q 253477. Q 253477. Q 25347. 
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W09325713-A.
23-DEC-1993.
17-JUN-1993. U05857.
17-JUN-1992. US-9006.
16-DEC-1992. US-9012.
(ARCH-) ARCH DEV CORU
D1az MO, Rowley JD;
WPI; 94-007568/01.
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Q53477;
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                         Detecting
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Sequence 14255 BP;
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                                                                                                                                                                                                                             Leukaemia; leukemia; MLL
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                         MLL
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US-991244.
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RESULTI Q75181, ID Q75181, Q75
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Best Loc
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24-SEP-1992; US-954112
30-SEP-1992; US-954112
13-MAY-1993; US-061376
13-MAY-1993; US-061376
(SALK) SALK INST BIOLOGICAL ST
Djabaki M. Evans GA, Parry P,
WPI; 94-135206/16
                                                                   075181 standard; cDNA; 14255 BP.
075181;
18-AUG-1995 (first entry)
ALL-1 (acute lymphocytic leukaemia-1) cDNA.
Acute lymphoblastic leukaemia; acute nonlymphoblastic leukaemia; chromosomal translocation; abnormality; detection; t(4:11); t(9:11); t(11:17); ALL-1; AF-4; AF-9; AF-17; chimeric gene; prob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding a human tri:thorax protein - used to develop agents for diagnosis and treatment of diseases associated with disruption of chromosome II at q23 Claim 4; page 36-42; 68pp; English.

In the course of the construction of a physical map of human chromosome region 11q23, a region cond the t(4:11) translocation breakpoint was cloned. The cloned DNA encoded a protein homologous to the diagnosis and treatment of immunodeficiency states, developmental abnormalities, inherited diseases or cancers, e.g. acute lymphocytic leukaemia or acute myelomonocytic leukaemia. Sequence 11907 BP; 3469 A; 2990 C; 2735 G; 2709 T;
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The sequence is that of cDNA clone 14P-18B, derived from the ML gene and used as a probe in a method for detecting leukaemic ce containing 11q23 chromosome translocations. The method is usefu in the diagnosis and monitoring of certain types of leukaemia using northern and Southern blot analysis and fluorescence in situ hybridisation (FISH). The probe detects rearrangements in dividing leukaemic cells and interphase nuclei.

sequence 4201 BP; 1273 A; 996 C; 989 G; 943 T;
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27-SEP-1994 (first entry)
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  Location/Qualifiers 3901. .4032
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US487970-A.

US487970-A.

D 30-JAN-1996.
F 17-JUN-1992; 900689.
F 17-JUN-1992; US-900689.
R 17-JUN-1992; US-901244.
R 16-DEC-1992; US-901244.
R 17-JUN-1993; US-080255.
A (ARCH-) ARCH DEV CORP.
D1az MO, Rowley JD;
R WPI; 96-105221/11.
F Detection of 11q23 chromosome translocation(s) - usi 1 eukaemia nucleic acid probes, for diagnosis and mor 1 eukaemia (s) and lymphoma(s)
S Claim 9; Column 43-44; 47pp; English.
C T16329 and T16330 are human genomic DNA sequence der (myeloid/lymphoid leukaemia) gene. The sequences are
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New acute lymphocytic leukaemia gene prods. - used for the diagnosis and treatment of leukaemias, partic. acute lymphoblastic or nonlymphoblastic leukaemia Claim 65; Page 62-79; 207pp; English.

The ALL-1 cDNA was obtained from a series of overlapping clones spanning 14.7 kb, isolated by screening a human fibroblast libra and a K562 library. The sequence revealed a single, long ORF predicting a protein of approx. 4000 amino acids. The predicted amino acid sequence includes regions of homology with the Drosophila trithorax gene which contain zinc-finger domains. The ALL-1 gene on chromosome 11 is involved in a series of chromosomal translocations which are associated with certain
                                                                                                                                                                                                                                   29-JUL-1997 (revised)
06-JUN-1996 (first entry)
06-JUN-1996 (first entry)
MLL 1.5EB fragment for detecting 11q23 chromosome translocations.
MLL; myeloid; lymphoid; leukaemia; probe; chromosome; translocati
mutation; 11q23; lymphoma; diagnosis; monitoring; ss.
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T16330;
29-JUL-1997 (revised)
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1. .11733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "nucleotides 9353-9696 were found nearly identical to an anonymous sequence (EST00626) cloned from human foetal brain cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4067 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rimers for amplifying chimeric sequences derived from this region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.2; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3542 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplifying chimeric rom this region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3215 G;
      derived from the MLL are used as probes
                                                           using myeloid/lymphoid monitoring of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                        translocation;
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RESULT 1
T58840_0
WP Sequen
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                                                                                                                                                         PT Detection of 11q23 chromosome translocation(s) - using myeloid/lymphoid PT leukaemia nucleic acid probes, for diagnosis and monitoring of PT leukaemia(s) and lymphoma(s) PT leukaemia(s) and lymphoma(s) PT leukaemia(s) and 11ymphoma(s) PS Claim 12; Column 43-48; 47pp; English.

CC Clones 14-7 and 14-18B. The clones are used as probes for 11q23 CC chromosome translocations associated with various human leukaemias.

CC Hybridisation of the probes to aberrant sized DNA segments is CC indicative of an 11q23 chromosome translocation. The probes are CC useful for the diagnosis and continued monitoring of various types CC inducation. The clones may also be used for protein prodn. (see R92705 and R92706) and hence antibody prodn.

CC (Revised entry submitted to correct sequence analysis breakdown.)

SQ Sequence 4201 BP; 1273 A; 996 C; 989 G; 943 T;
                                                                                                       Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 18
  Sequence
                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1992;
16-DEC-1992;
17-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                               US5487970-A.
30-JAN-1996.
17-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemias. Hybridisation of the probes to aberrant sized DNA segments is indicative of an 11q23 chromosome translocation. The probes are useful for the diagnosis and continued monitoring of var types of leukaemia, partic. myeloid and lymphoid leukaemias and lymphomas in humans. The probes may also be used for protein prodn. and hence antibody prodn.

(Revised entry submitted to correct sequence analysis breakdown.) Sequence 1420 BP; 451 A; 323 C; 348 G; 298 T;
                                                                                                                                                                                                                                                                                                                                            (ARCH-) ARCH DEV CORP.
Diaz MO, Rowley JD;
WPI; 96-105221/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1996 (first entry)
MLL cDNA clone 14-18B for detecting 11q23 chromosome translocations.
MLL; myeloid; lymphoid; leukaemia; probe; chromosome; translocation; mutation; 11q23; lymphoma; diagnosis; monitoring; ss.
                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1997
06-JUN-1996
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                                                                                                                 Local Similarity
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                                                                        atgaaaaggaaagctaaaagt
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  split
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18; Conservative
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US-900689.
US-991244.
US-080255.
  into
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2. .4201
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  fragments
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85.78;
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85.7%;
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Pred. No. 1.
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Pred. No. 1
  LOCUS T58840 Accession
                                                                                                       Mismatches
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                                                                                                    DB 1;
1.3e+02;
nes 3;
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  megabase shotgun sequencing method; open reading frame; Mycoplasma genitalium.
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Key
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M. genitalium; DNAA; |
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158840_0
158840_1
158840_2
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158840_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein covered GB:D26185_102" 12069. .12725
                                                                                                                                                                                                                                                                                                                                            /note= "Previously identified encoded protein shows 31.50 periodentity to the ribosomal proteins."
                                                                                                                                                                                                                                                                                                                                                                                                   encoded protein shows 25.73 percentage identity to DNA primase (dnaE) from Clostridium acetobutylicum" complement (13570...14247)
/label= MG024
/note= "Previously identified as MORF-19826
MORF-20093, the encoded protein shows 46.84
percentage identity to GTP-binding protein
from E. coli"
                                                                                                                                                encoded protein shows identity to transport (msbA) from E. coli" 26478. .27344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 8552. .9184
                                                                                                               /*tag= g
/label= MG023
/note= "Previously
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/note= "Previously
                                                                                                                                                                                                                                                                                                              complement (14396. .15217)
                                                                                                                                                                                                                                                                                                                        coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "Previously
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; 580073
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110000
210000
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580073
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protein s6
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and MORF-20081, the encoded protein shows 33.04 percentage identity to 5,10-methylene-tetra-hydrofolate dehydrogenase (folD) from E. coli" 17474. .19243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= MG009
/label= MG009
/note= "Previously identified as MORF-20078, the encoded protein shows 35.43 percentage identity to the Bacillus subtilis hypothetical protein covered in accession number
                                                                                                 /note- "Previously identified as MORF-20092, encoded protein shows 45.96 percentage identity to fructose-bisphosphate aldolase (tsr) from B. subtills"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= MG006
/note- "Previously identified as MORF-20076,
noted protein shows 27.59 percentage
encoded protein shows 27.59 percentage
identity to thymidylate kinase (CDC8)
from Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= MG013
/note= "Previously identified as MORF-19823,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modification protein (rimK) from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identified as MORF-20079,
ows 25.73 percentage
                                                                                                                                                                                                                                                                                                                                                                                          identified as MORF-20084,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as MORF-20080,
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                                                                           /label= MG043
/note= "Previously identified as MORF-20110,
/note= "Previously identified as MORF-20110,
encoded protein shows 26.51 percentage
identity to spermidine/putrescine transport
system permease protein (potB) from E. col1"
     /label= MG044
/label= MG044
/note= "Previously identified as MORF-20111, the encoded protein shows 29.45 percentage identity to spermidine/putrescine transport system permease protein C (potC) from E. coli"
                                                                                                                                                                                                                              /note= "The encoded protein shows 48.86 percentage identity to phosphohistidinoprotein-hexose phosphotransferase (ptsH) from Mycoplasma capricolum"
                                                                                                                                                                                                                                                                                                                                                                   /label- MG038
/note- "Previously identified as MORF-20105, note- protein shows 46.83 percentage identity to glycerol kinase (glpK) from E. coll "
                                                                                                                                                                                                                                                                                                  /note- "Previously identified as MORF-19831 MORF-20106, the encoded protein shows 43.20 percentage identity to glycerol-3-phosphate dehydrogenase (GUT2) from S. cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                              encoded protein shows 30.71 percentag
identity to histidyl-tRNA synthetase
from Mycobacterium leprae*
complement (44751. .46277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note "Previously identified as MORF-20101, encoded protein shows 48.13 percentage identity to thymidylate kinase (tdk) from B. subtills"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded protein shows 35.90 identity to glycerol uptake (91pF) from B. subtilis"
                                                                                                                                                                       MORF-20108, the encoded protein sh percentage identity to spermidine/
                                                                                                                                                                                                                                                                                           dehydrogenase
49377. .49643
                                                                                                                                                                                                                                                                                                                                                           complement (46268. .47422)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40543. .41787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Previously identified as MORF-20099,
encoded protein shows 26.82 percentage
identity to ATP-dependent nuclease (addA)
from B. subtilis"
39242. .39904
                                                                                                                                                    putrescine transport ATP-binding
(potA) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- MG035
/note= "Previously identified as MORF-20102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Previously identified as MORF-20100,
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                                                                                                                                                                                "Previously identified as MORF-19832 0108, the encoded protein shows 41.92
                                                                          permease
.53220
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мс043
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МG042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            percentage
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                                                                                                                                                               protein
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Matches 18
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                                            10-NOV-1997 (first entry)
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                                                              standard;
                                                                                                                                                              Similarity
                                                                                                                                                     Conservative
                                                                                                                                                                                                                               (SPase)
91065. .
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/note= "Previously identified as MORF-20112,
/note= "Previously identified as MORF-20112,
encoded protein shows 36.60 percentage
identity to sialoglycoprotease (gcp)
from Pasteurella haemolytica"
complement (56970. .58310)
                                                                                                                                                                                          encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subtilis"
                                                               DNA;
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                                                                                                                                                             77.18;
85.78;
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RESULT
T51257/
ID T59
AC T59
DT 10
DT 10
DE HU
KW AU
KW NG
KW NG
KW NG
                Human AD4 gene genomic sequence stm.genD.
Autosomal dominant early-onset Alzheimer's Disease; AD4;
neurodegeneration; senile dementia; human chromosome 1;
Volga German kindred; VG; ss.
                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= MG067
/label= MG067
/note= "previously identified as MORF-19845,
/note= "previously identified as MORF-19845,
encoded protein shows 28.84 percentage
identity to glutamic acid specific protease
identity from Staphylococcus aureus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Previously identified as MORF-: encoded protein shows 38.90 percentage identity to the protein disclosed in GB:D26185_104 from B. subtilis" 81047. .82597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded protein shows 30.25 percent identity to the protein disclosed i GB:D26185_99 from B. subtilis" complement (65713. .66249)
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/note- "Previously identified as MORF-20114
MORF-20115, the encoded protein shows 44.78
percentage identity to purine-nucleoside
phosphorylase (deoD) from E. col1"
59083. .59754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Previously identified as MORR-19834, MORF-20114 and MORF-20115, the encoded protein shows 43.02 percentage identity to signal recognition particle protein (ffh) from B.
                                                                                                                                                                                                                                                                                                                                                                          /*tag= z
/label= MG070
/note= "Previously identified as MORF-20136,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- MG057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Previously identified as MORF-20122,
                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                from .91919
                                                                                                                           ₽₽
                                                                                                                                                                                                                   24649
                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                       Score 16.2; DB 1; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                             shows
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                             34.8
                                                                                                                                                                                                                                                                                                                                                           percentage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as MORF-20123,
                                                                                                                                                                                                                                                                                                                        Length 110000;
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Search completed: August 18, 1999, 17:18:31
Job time: 3263 sec
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                                                                                                                                                                                                                                                                                         PI Bird TD, Galas DJ, Levy-Lahad E, Mulligan J, Schellenberg GD;
PI Tanzi RE, Wasco W;

DR WPI; 97-119048/11.

DR WPI; 97-119048/11.

New Alzheimer's disease related gene, AD4 - used to develop prods.
PT New Alzheimer's disease related gene, AD4 - used to develop prods.
PT for detecting pre-disposition to or for diagnosis, prevention or
PT treatment of Alzheimer's disease
PS Claim 46; Fig 16; 83pp; English.

CC Agenetically isolated group of families with autosomal dominant
CC early-onset Alzheimer's Disease (AD) (the Volga German kindreds) has
CC AD4 gene was amplified from YAC 921d12 DNA and was radiolabelled by
CC AD4 gene was amplified from YAC 921d12 DNA and was radiolabelled by
CC AD4 gene was amplified from YAC 921d12 DNA and was radiolabelled by
CC inick translation. A human genomic clone hybridising to this fragment
CC was identified in a commercially available library. The clone carried
CC the entire AD4 gene and was sheared and subcloned into Mi3mpl8 vector
CC for sequence analysis. The sequences of the 12 exons and the flanking
CC intron sequences of the AD4 gene were determined. The present sequence
CC includes exon 5. Mutations in the AD4 gene, identified in Volga German
CC kindreds, are associated with Alzheimer's Disease, especially a
CC mutation at codon 141 which replaces Asn by Ile. Detection of mutant
CC AD4, for example using antibodies specific for the provides a means of
CC diagnosing Alzheimer's disease.

SQ Sequence 1438 BP; 319 A; 398 C; 346 G; 375 T;
                                                                                                                                                                                         Query Match 77.3
Best Local Similarity 85.3
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09703192-A2.
30-JAN-1997; U11386.
14-AUG-1995; US-002328.
17-JUL-1995; US-00956.
28-JUL-1995; US-001675.
11-AUG-1995; US-002174.
(DARW-) DARWIN MOLECULAR CORP.
(GEHO) GEN HOSPITAL CORP.
(YAME-) VA MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Кеу
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964 AGGAAAAGGAAAACTAAAAAT 944
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/note= "Approximate position; determined fr
listed in Table 4 of the specification and
comparison with cDNA sequence in T51254"
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157. .300
                                                                                                                                                                                         77.1%; Score 16.2; DB 1; 85.7%; Pred. No. 1.2e+02; Live 0; Mismatches 3;
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                                                                                                                                                                                                                                 Length 1438;
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Sequence:
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21
1 atgaaaaggaaagc
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em_est5: *
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53.996 Million cell updates/sec
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| 57 :<br>58 :             | 56:        | 55:        | 54:        |
|--------------------------|------------|------------|------------|
| em_est25:*<br>em_est26:* | em_est24:* | em_est23:* | em_est22:* |

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Result 000 000 000 a 0 0 000 a 0000 ŏ Score Query Match Length BB AA514077 R19941 T187926 D62554 D62554 A73600 AA700025 AA1971083 A1371083 A137160 AA0032576 AA0025762 AA16406 AA052378 AA06463 W92378 W92378 W92378 AA406425 AA16406425 AA164064 AA0588463 W92378 W92378 AA406425 AA16406425 AA16406425 AA164064 AA0588463 W92378 W92378 W92378 W92378 W92378 AA406425 AA16407 AA406425 AA16406425 AA16406425 AA16406425 AA1653051 ID SUMMARIES AA514077 MC2AS032. R19914 Y9306702.rl T87926 ye08c06.rl T87926 ye08c06.rl D62554 HUM300B06B D63016 HUM352DD7B N73600 ZE51606.2s AA987196 or92all.s AA700025 Zi69d12.s AA987196 or92all.s AI17933 ESTZ2309.x AI158916B tf81h04.x T95759 ye40d12.rl N29345 yw85c10.sl AA009986 Ze166410.rl N29345 yw85c10.sl AA009986 Ze166410.rl N29345 yw85c10.sl AA009986 Ze166410.rl N7287762 AV025762 AV025762 AV025762 AV025762 AV025762 AV025762 AV025761.s AA0648643 Zd336e07.rl N728842 Zf64bb04.s AA164407 Zo97h11.s AA4646425 Zv12c11.rl N68463 Zd336e07.rl N92378 Zd99912.sl AA064407 Zo97h11.s AA464047 Zo97h11.s AA464047 Zv12c11.rl N68463 Zv12c11.rl N684663 Zv12c11.rl N68466 Zv2c03.rl N684660 Zv2c03. Description

## ALIGNMENTS

| NID<br>VERSION                    | ACCESSION                                    | DEFINITION      | LOCUS                                | AA514077 | RESULT 1 |
|-----------------------------------|----------------------------------------------|-----------------|--------------------------------------|----------|----------|
| 92252933<br>AA514077.1 GI:2252933 | cDNA clone AS-32 5', mRNA sequence. AA514077 | ambda Zap Schis | AA514077 211 bp mRNA EST 10-JUL-1997 |          |          |

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BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
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SOURCE
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AUTHORS
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LOCUS
DEFINITION
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 R19941 428 bp mRNA EST 17-APR-1995 yg30f02.rl Soares infant brain INIB Homo sapiens cDNA clone IMAGE:33933 5' similar to contains Alu repetitive element; contains L1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 428)

1 (lark,N., Dubuque,T., Elliston,K., Hawkins,M., Hillier,L., Clark,N., Dubuque,T., Elliston,K., Marra,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Pargaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
On May 18, 1
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Schistosoma mansoni.
Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schistosome Gene Identification
Unpublished (1997)
On May 18, 1995 this sequence v
                Email: est@watson.wustl.edu
Insert Size: 1657
                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                      Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                              Unpublished
                                                                                                                                                                                 The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                     R19941.1 GI:774575
EST.
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Location/Qualifiers
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Fax: (202)2853561
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                                                                                                                              Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                      human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Karim, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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quality sequence stops:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Schistosoma mansoni"
/db_xref="taxon:6183"
/clone="AS-32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Library provided by Dr. M.
36 c 51 g 63 t
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95.0%;
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                                                                                      School of Medicine way, Box 8501, St. 1
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Pred. No. 3
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235 Source:
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                                                                                        Louis,
IMAGE Consortium, LLNL
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RESULT
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| |||||| |||||||||||
                                                                                                                                                                                                                                                                            Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 397)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Chissoe, S., Hultman, M., Rucaba, T., Le, M., Le, M., Le, N.,
Hawkins, M., Hultman, M., Rucaba, T., Le, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
and Marris, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9716278
T87926.1
Email: est@watson.wustl.edu
Insert Size: 641
High quality sequence stops: 179 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1657 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 235.
                                                                                                                                  Washington University Scho 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ye08c06.rl Stratagene
IMAGE:117130 5', mRNA
                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                          Contact: Wilson RK
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                                                                                                                                                                                                                                                 Generation
                                                                                                                                                                                                                                                                    and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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/db_xref="GDB:406280"
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Pred. No. 5.6e+02;
0; Mismatches 2;
                                                                                                                                  School of Medicine way, Box 8501, St. Louis,
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1 (bases 1 to 401)

Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.

Fujiwara et al. (1995)

Unpublished (1995)

On Apr 14, 1993 this sequence version replaced gi:693411.
  l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                            otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho,
Tel: 0886-65-2888
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Seq primer: M13RP1
High quality seque
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Location/Qualifiers
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                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="1p"
/clone="GEN-300806"
/clone_lib="Clontech human a
64 c 61 g 149 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="72 years"
//lab_host="SOLR cells (kanamycin resistant)"
//lab_host="SOLR cells (kanamycin resistant)"
//note="Organ: lung; Vector: pBluescript SK-; Site_1:
//note="Organ: lung; Vector: pBluescript SK-; Site_1:
//note="Site_2: XhoI; Cloned unidirectionally. Primer:
//note="Site_2: XhoI; Cloned unidirectionally. Primer:
//note="Site_2: XhoI; Cloned unidirectionally. Primer:
//note="Site_1: Analysis of the control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 bp mRI
B Clontech human a
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/clone="IMAGE:117130"
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Pred. No. 5.7e+02;
0; Mismatches 2;
Score 17.8; DB 23
Pred. No. 5.7e+02;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, T
Tel: 0886-65-2888
Fax: 0886-37-1035
                                                                                                                                                                                                                                         g1230885
N73600.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 296)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. an
                                                                                                                                                                                                                                                                                                                               N73600 296 bp mRNA za51d06.s1 Soares fetal liver spleen lNF IMAGE:296075 3' similar to contains Alu
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Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Indiano,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.
Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai Maekawa,H., Shin,S. and Nakamura,Y.
Fujiwara et al. (1995)
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="932A02; 2; 2242.3-2q31.3 (2q31)"
/clone="GEN:352D07"
/clone_lib="Clontech human aorta polya+ mRNA (#6572)"
a 62 c 57 g 131 t
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1. .355
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90.5%;
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Pred. No. 5.8e+02;
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INFLS Homo sapiens cDNA clone
Alu repetitive element;, mRNA
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AA700025
                                                                                                                                                                       WashU-NČI human EST Project Unpublished (1997)
On Sep 12, 1996 this secure.
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 217)

1 (bases 1 to 217)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R.
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On Oct 18, 1995 this sequence version replaced gi:1026892.
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 212.
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Fax: 314 286 1810
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                                                                                                         Contact: Wilson RK
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
// Stranded cDNA was primed with a Pac I and cloned into the Pac I
// Stranded cDNA was ligated to Eco RI adaptors
// (Pharmacia), digested with Pac I and cloned into the Pac I
// and Eco RI sites of the modified pT7T3 vector. Library
// went through one round of normalization. Library
// constructed by Bento Soares and M.Fatima Bonaldo."
// Stranded CDR (B) G6 t
// Stranded CDR (B) G6 t
// Stranded CDR (B) G7T3 vector.
// Stranded CDR (B) G
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/clone="IMAGE:296075"
/clone_lib="Soares fetal liver spleen lNFLS"
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/db_xref="GDB:1240996"
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Pred. No. 6e+02;
0; Mismatches
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                                                                                                                                                                    replaced gi:1290797
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: -40ml3 fwd. ET from AmerSham
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 th
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AA987196
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Location/Qualifiers
                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 414)
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                                                                                                                 Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/lab_host="PHIOB (ampicillin resistant)"
/note="Organ: Liver and Spleen: Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
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/db_xref="GDB:1335824"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                 replaced gi:2044427
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                                         information can be
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19; Conserv
                                                                                                                                                                                                                                       The Institute for Genomic Research 9712, Medical Center Drive, Rockvi Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
On Aug 21, 1998 th
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AI179333.1
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciuroqnathi; Muridae: Murinae.
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              /note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
a 152 c 171 g 124 t
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/db_xref="taxon:9606"
                                                                                                 /organism="Rattus sp."
/db_xref="ATCC (inhost):2035046"
/db_xref="taxon:10118"
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/tissue_type="carcinoid"
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                                                                                    /clone="RSPCF39"
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                                                                /clone_lib="Normalized rat spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:3729971
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                                                                                                                                                                                                                                                                                                                                            this sequence version replaced
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                                                                                                                                                                                                                                                                                                                                                                                              Generation of a Rat
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                                                                                                                                                                                                                                                         MD 20850, USA
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                                                                  Bento Soares*
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REFERENCE
AUTHORS
TITLE
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DEFINITION
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Query Match
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Matches 19; Conserv
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||||| |||||||||| |||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 491)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer:
High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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AI371083.1 GI:4149836
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AI371083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan.
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                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                    primer: ~400P from Gibco quality sequence stop: 417. Location/Qualifiers
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                                                                                                             /db_xref="taxon:9606"
/map="7432; D7S686-D7S640"
/clone="IMAGE:2043401"
/clone_lib="NCI_CGAp_Brn23"
/clone_lib="NCI_CGAp_Brn23"
/tlssue_type="q1ioblastoma (pooled)"
/lab_host="DH10B"
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Pred. No. 5.3e+02;
0; Mismatches 2;
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Conservative

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Score 17.8; DB 45 Pred. No. 5.5e+02; 0; Mismatches 2

DB 45;

Length 491;

Indels

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     RESULT 12
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Best Local S
Matches 19
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                                                                           ATGAAAAGGAATGCTAGAAGT 462
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19; Conser
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Unpublished (1997)
On Jun 5, 1998 this
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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AI478812
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI478812 511 bp mRNA EST 14-APR-1999 tm52f03.xl NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2161757 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                                                                                                       195
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                               /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "3 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
/db_xref="taxon:9606"
/map-"89001; 5: 5923.2-5931.1"
/clone="IMAGE:2161757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Kidl1"
/lab_host="DH10B"
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                                                                                                                                                            84.8%;
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                                                                                                                                             Score 17.8; DB 47; pred. No. 5.5e+02; 0; Mismatches 2;
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                                                                                                                                                                               Length 511;
                                                                                                                                            Indels
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                                                                                                                                             Gaps
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                                                   RESULT 13
AI694973
LOCUS
DEFINITION
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DEFINITION
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AUTHORS
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ORGANISM
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KEYWORDS
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Best Local Similarity
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mRNA sequence.
AI694973
g4982873
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1 atgaaaaggaaagctaaaagt 21
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1 (bases 1 to 506)

NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

On Mar 10, 1998 this sequence version replaced gi:2948176.
A1694973 442 bp r
we44h08.xl NCI_CGAP_Lu24
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Seq primer: -40UP from Gibco
High quality sequence stop: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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AI589168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop:
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:2105719"
/clone_11b-"NCI_CGAP_Brn23"
/tissue_type-"glioblastoma (pooled)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
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                                                                                                                                                                                                                        84.8%;
                                                                                                                                                                                                    0;
                                                                                                                                                                                                  Score 17.8; DB 48; Pred. No. 5.5e+02; 0; Mismatches 2;
    mRNA
4 Homo
    EST
sapiens cDNA clone
                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                        Indels
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    03-JUN-1999
IMAGE:2343999 3',
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 395)
                                                                                                                                                                                                           T95759 395 bp mRNA EST ye40d12.rl Soares fetal liver spleen lNFLS image:120215 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
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1 (bases 1 to 442)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2343999"
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   Clark,N., Dubuque,T.,
Hultman,M., Kucaba,T.,
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Pred. No. 5.6e+02;
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Insert Size: 1325
High quality sequence stops: 298 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 298.
                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 467)

1 (bases 1 to 467)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                               N29345 467 bp mRNA EST 05-JAN-1996
yw85c10.sl Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
clone_IMAGE:259026 3', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:810992.
                                                The WashU-Merck EST Project
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/db_xref="GDB:472760"
/db_xref="taxon:9606"
/clone="IMAGE:120215"
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| ACUU6622 CEY116A8_3 CEY116A8_4 CEY43D4_0 HS620E11 HSDJ137K2 ACUU353 PFALSA1A PFALSA1B PFALSA1B PFALSA1B PFALSA1B PFALSA1G CELR160 PFALSA1C | BBU62900<br>HSBA55N20<br>HSBA55N20<br>HSBA75N20<br>HSBA77H23<br>HSBA107C2<br>HS353E16<br>HS692C8<br>PIP404CG<br>U67501<br>HSBA69CB<br>U67501<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSBA69CB<br>HSB |
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## ALIGNMENTS

| JOURNAL                                          | TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                | REFERENCE<br>AUTHORS                                                                                                                                                                                                                          | VERSION VERSION KEYWORDS SOURCE ORGANISM                                     | AE001168 LOCUS DEFINITION ACCESSION                                                                                           |
|--------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| DurgdoTier1<br>Nature 390 (6660), 580-586 (1997) | Gwinn, M. Dougherty, B. Tomb, J. F. Fleischmann, R.D. Richardson, D., Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S., Hanson, M., van-Vugt, R., Palmer, N., Adams, M.D., Gocayne, J.D., Weidman, J., Utterback, T., Watthey, L., McDonald, L., Artiach, P., Bowman, C., Garland, S., Fujii, C., Cotton, M.D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C. Genomic sequence of a Lyme disease spirochaete, Borrelia | Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group. 1 (bases 1 to 13271) 1 (bases, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R.A., Lathiora, R., White, O., Ketchum, K.A., Dodgon, R., Hickey, F.K. | 92588598 AE001168.1 GI:2688598 Lyme disease spirochete. Borrelia burgdorferi | AE001168 13271 bp DNA BCT 15-DEC-1997<br>Borrella burgdorfer1 (section 54 of 70) of the complete genome.<br>AE001168 AE000783 |

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FEATURES
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EIFRAAHTLKGSSASLDMMELGDFTHIVEDVFDAIRDGKVINNDLVDLLLSSLDVIK
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EGNVISIELEDDGIGIDPKVIRKLIEKGTIKEDAIYSDFELINLIFAGFFSTAVQVT
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Location/Qualifiers
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1168. .3762
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66. .1100
                                                                                                                       /gene="BB0670"
3769. .5169
                                                                                                                                                                                                                                                                   DLSGRGVGLDVVKKSIEKLNGTILVESEIGLGTIFKIKLPLTLVIIQGLLVKSGSETY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="chemotaxis histidine kinase (cheA-2)"
/protein_id="AAC67024.1"
/db_xref="plb:92688607"
/db_xref="G1:2688607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to PID:1113815 SP:044737 GB:AE000783 percent identity: 99.31; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC67025.1"
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                                                                                                                                                                                                         DLQKDTKE"
                                                                                                                                                                                                                                        VYNTSNMKIAIVVDSILGEEDFVVKPIKDKFSSSAGIVGATTLGNGKVVLIIDVFKLF
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/note="similar to
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identified by sequence similarity; putative"
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codon_start=1
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                                                          note="similar to
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                                                                                                                                                                                 .5169
                           GP:1881576 percent identity:
uence similarity; putative"
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VIMISALGKEQLVKDCLIKGAKTFIVKPLDRAKVLQRVMSVFVK"
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5181. .5666
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NLMGADCLEEFKNEIYESFLSFMNNLKSIFNVLEFGCGSGKETMALALSEYVKFF
KLTALDNDLSKVVETGRLVFSESEIGISEIYSRNSFEDSFGVYKFKSEILSNVLEYSS
DALFSDLPDNLGMVFLKDVLCFLDSKDQILIINIIASKAIKGALLVLGDNEELKNNDV
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gvrelrkssnrtyvphakkyvagldnlegeiipiidlaimenlephkkoiedimylkn
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/db_xref="GI:2688610"
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/gene="BB0674"
                                                                                                                                                                                                                                                                                                        complement (6699.
/gene="BB0674"
                                                                                                                                                                                                                                                                                                                                                                                            FLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNITYFLKNLDK
                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKIQIIIMLLALLDFPLNARLLDISIEKRADEEIKKYSSYNLIL
| EKEYYTNFPTSEIEKNIYKLTEHFYKSIMLNKTNYSLLNSNYKEANKYLIQSELIDKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6187. .6702)
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/protein_id="AAC67021.1"
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/protein_id="AAC67022.1"
/db_xref="PID:92688605"
/db_xref="GI:2688605"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="G1:2688604"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="BB0672"
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                                                                                                                                                                                                                                                                                                                                                               SNEMIFFPRE"
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gene

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Query Matcn
Best Local Similarity
Matches 19; Conser
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Borrelia burgdorferi flagellar filament outsheath protein
gene, complete cds, and chemotaxis histidine kinase (cheA)
                                                                                                                             Submitted (03-JUL-1996) Yigong Microbiology, HSCN, Morgantown,
                                                                                                                                                                                                                              J. Bacteriol. 179 (2), 97144545
                                                                                                                                                                                                                                                                        burgdorferi
                                                                                                                                                                                                                                                                                                              Ge, Y. and Charon, N.W.
                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia
                                                                                                                                                                      Direct Submission
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1 (bases 1 to 1655)
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PID:1222502 PID:1204815 percent identity: 25.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8599. .9261)
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frikndfeseikblio?ykbkydimirppylsoieaideniykpylskeltknblnli
fnyykvnsslakeffynfntisngylipyinklebeknsytiyllokenkalyssbi
knyikilllkvlvikycfekgielftkniestskaisndtdfldektakiliesffk
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/gene="BB0675"
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TILNPIMLSLFKLFFLEKLFFNDLIIFIZYVRSKEKILILIAFAATFSMSLLIPFTFFI
IISSSKIVNSIPEKQEFNIIKNISIINEKAYIKEKYPFILIIKEKDDIIYKSKDEHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:1575445
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                                                                                                          Location/Qualifiers
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/trans1_table=11
          /clone-"pW1 and pW2"
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Pred. No. 1.3;
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                                                                                                                             West Virginia University, 26506, USA
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protein (flaA)
se (cheA) gene,
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AUTHORS
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DEFINITION
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Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                in unordered AL078632
                                                                Ainscough, R.
Direct Submission
                                                                                                                          Eukaryota;
Eutheria; F
                                                                                                                                                                                                        AL078632.1 GI:5051845
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                  Homo sapiens
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/gene="cheA"
1566. .>1655
/gene="cheA"
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/protein_iable=11
/protein_iable=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKRKAKSILFFLLSTVLFAQETDGLAEGSKRAEPGELVLDFAEL
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DNIKTMKEIKYSVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFGWADLIWSNPNYIP
NISSRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKVKNEIFYVKDLRVLYDKLSVSID

    395
    function-"unknown"

                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo. 1 to 175001)
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182 c 308 g 605 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="CheA protein"
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/db_xref="GI:1575448"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDIDSESVFKVYETSGTESLRKLKAHETFKRVLKLREKISIAEGSFQNFVEKIESEKP
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473. .1498
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/function="putative flagellar filament outsheath protein"
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                    Human DNA sequence from clone 477H23 on chromosome 22q12.1-12.2. Contains parts of one or two novel genes. Contains ESTs and GSSs, AL033538
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IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
Homo sapiens
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               AL033538.1
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/db_xref="taxon:9606"
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22 clone BA9F11, WORKING DRAFT SEQUENCE,
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This sequence is the entire insert of clone 477H23. The true left end of clone B107C2 (AL008724) is at 12724 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-JAN-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477H23 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://Dacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
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/note="L1M4 I
8497.
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/note="L1ME repeat:
4872. .5181
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/note="AluSg repeat:
4075. .4377
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/db_xref="taxon:9606"
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/note="LlMEC repeat:
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/note="L1MC4 repeat:
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SIASSMSFVSKPEGGSEGGPGGRQDHDRSKNAYLQRSTLPRSQLPQTRPAGNKDEE
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VTYKFKPPARSSSLPKVSSGYSSFTTSEMSIKDSPSQHSGRPSPGCDSQTSQLDQPLF
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14910. .15059
/note="LIM4 repeat: matches 3034. .3203 o
/note="LIM4 repeat: matches 2<7"
15814. .15956
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/note="LlME2 repeat: 10258. .10357
/note="LlME2 repeat: 10258. .1027. repeat: 10258. .10357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1M4 repeat: 16140. .16323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10921. .11355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="dJ477H23.1"
complement(17058)
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/product="dJ477H23.1 (nove
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13956. .14086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .29120)
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Human genomic DNA sequence from
22q11.2-12.1. Contains ESTs and
                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
Submitted (29-DEC-1997) Chromosome 22 Project Group (http://www.sanger.ac.uk/HGP/Chr22/) Sanger Centre, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.
                                                   Direct Submission
                                                                                                                                   Homo sapiens
                                                                                                                                                                                   AL008724.1 GI:2760024
                                                                                  (bases 1 to 44665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 1. complement(25826. .26207)
/gene="dJ477H23.1"
/note=""""
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LPSGNGYKFLSPGRFFPSSKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental /product="du477H23.2 (novel protein)" /protein_id="CAB37645.1" /db_xref="pID:e1390400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the same gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: proteins Q55489 P74108; match: ESTs D31449
H55314; presumably this gene and dJ477H23.1 are part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(<35280. .35303,37584.
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complement(35280. .40597)
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/db_xref="GI:4467801"
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26494. .26764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="GLMHSSGPVGRHRQLILVLEGELYLIPFALLKGSSSNEYLYERF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="FLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                     86.3%;
94.4%;
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Pred. No. 3
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/note-"LIMA2 repeat: matches 1055. .782 of consensus" prim_transcript 4335. .5562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Otto: 1.75/3 mer 100 % conserved prim_transcript 7592. .8329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prim_transcript complement(7040. .7546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B107C2 is from the human chromosome 22-specific cosmid library (SC22cB) constructed at the Sanger Centre by Mark Ross and Cordelia Langford, VECTOR: Lawrist 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within know annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping group.

Further information can be found at http://www.sanger.ac.uk/HGP/Chr22/.
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IMPORTANT: This sequence is the entire insert of clone B107C2. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was generated from part of bacterial clone contigs human chromosome 22 constructed by the Sanger Centre chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The true left end of clone B107C2 is at 1 in this sequence. The true right end of clone B107C2 is at 44665.
                                                                                                                                                                                                                                                                                                                                                                         /notee match: ESTs AAA43013 R55269 H10978 AA359630; R55269 paired with EST K55270 matching this clone complement(10058 .16386)
/note="match: EST AA354647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: STS G06242"
5521. .5814
/note="AluSx repeat: matches 1. .296 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: ESTs AA393708 R58963 W26684 W76562 W72568 D60118 D60119 F11418 W25996 D80911 F01844 H61750 D60539 AA022630 AA010068 AA340208 H61749 H40968 D81868 AA116109 R61461 T35711 AA400907 T64146 R59018 F11011 R37806 T64274; poly-A tail on several clones at position 4335" 4343. 4585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2113. .2146
/note="17 copies of 2 mer
3417. .3675
                                                                                                                                                                                                                                                                                                 11605. .12279
                                                                                                                                                                                                                                                                                                                                                      10868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this clone 7546. .7573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5599. .6606
                                                                                                                                                                                                                                            /note="match: 12404. .12747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N25729"
/note="AluSp repeat:
15223. .15357
                                                                                                                                                           /note="AluJb repeat:
                                                                                                                                                                                                                /note="THE1C repeat:
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/clone="B107C2"
                                                                                                         mote≖"AluJb repeat:
                                                                                                                                                                                                                                                                                                                       note-"match: ESTs R19881 R13060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="FLAM_A repeat: matches 1. .132 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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                                                                        ncomplete repeat"
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                                                                                                                                                                                          .14026
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                           matches
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                           303.
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                                                                                                                                                                                                                   .371 of consensus"
                           .2 of consensus"
                                                                                                         of.
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                                                                                                         consensus;
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repeat:

matches

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.143 of consensus"

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HS353E16/c
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ORIGIN
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JOURNAL
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Best Local Similarity
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Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 12, 1999 this sequence version replaced gi:5042216.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
                                                                                                                                                                                                                                  HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                    unordered pieces.
AL031591
                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome
                                                                                                                                      Clark,G
                                                                                                                                                  Eutheria; Prima
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                     Homo sapiens
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38826. 3911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Alujo repeat: matches 281.
incomplete repeat"
44553, 44618
/note-"33 copies of 2 mer 94 % cor
11147 c 11427 g 10942 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: 40044. .40135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluJb repeat: matches 2. .287 of consensus" 37911. .37974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 96. 36055. .36128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: 29030. .29314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15857. .16056
/note="AluJb repeat: matches 200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR2 repeat: 41750. .42029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER2 repeat: matches 1. .160 of consensus"
37619. .37904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR2 repeat: matches 67. .146 of consensus"
37194. .37286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat:
incomplete repeat"
21955. .22082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="2 copies of 46 mer 99 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluJb repeat: matches 290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR •repeat: matches 204.
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Pred. No. 38
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22
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                                                                                                                                                                                                                                                                                                                  clone 353E16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 mer 94 % conserved"
10942 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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, WORKING
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HS692C8
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Best Local (
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|||||| || ||||||||
                                                                                                                                                                                                                                                                                               On Mar 22, 1999 this sequence version replaced gi:4455600. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence is the entire insert of clone 692C8. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An antempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                     http://www.sanger.ac.uk/HGP/Chr20
692C8 is from the library RPC14 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
Location/Qualifiers
                                                                                                                                                                                               This sequence was generated from part of bacterial clone contigs human chromosome 20, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-APR-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125698)
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                                                                                                                                                                                                                                                                                  feature key.
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ins STSs and GSSs, complete sequence.
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50625 c 49283 g
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                  1. .125698
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/db_xref="taxon:9606"
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94.4%;
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Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone 692C8 on chromosome
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/clone="692C8"
/map="p11.22-12.2"
/clone_lib="RPCI4"
       /note="L1MA5A
24791. .24890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17244 . 17532
/note="LTR16C repeat: matches
17666 . 18101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER47B repeat: matches 1. .418 of consensus"
16883. .17029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15514. .15575
/note="31 copies 2 mer
16460. .16868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1P repeat: matches 617. .2120 of consensus"
1501. .1586
/note="L1P repeat: matches 13. .98 of consensus"
                                                                                                                                                                                                                                                                                                       'note="L1ME3A repeat: matches 5279.
3656. .9173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MLT1H repeat:
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note="L2 repeat: matches 2527.
                                                                                                  'note="MER5B repeat: matches 2. .178 of consensus"
                                                                                                                                                                 'note="MIR repeat: matches 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER39b repeat: matches 429. .550 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LIPA8 repeat: matches 5642. .6161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MLT1H repeat: matches 285. .547 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MC4 repeat: matches 7466. .7968 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                      te="MSTC repeat: matches 1.
55. .19303
te="MIR repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4. .9373

te-"L1ME3A repeat: matches 5082. .5279 of consensus

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re="MERSA repeat: matches 10. .189 of consensus"
22. .11389
re="L2 repeat: matches 2674. .2742 of consensus"
11. .11752
re="MER39 repeat: matches 8. .380 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="L2 repeat: matches 2543. .2670 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 8655
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                                                                                                                                                                                                                                repeat:
                                   repeat: matches 6042.
                                                                                                                                                                                                                                       matches 2425.
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                                                                                                                                                                                                                                                                                                                                                                             .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .283 of consensus*
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                                                                                                                                                                     .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                            .401 of consensus"
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                                                                                                                                                                                                                                       .2745 of consensus"
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                               .6285 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MLT1H repeat: matches 29. .494 of consensus" 34345. .34663 /note="LM36 repeat: matches 10. .336 of consensus" 35259. .35554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 21. .121 of consensus" 26211. .2639 /note="LTR16A repeat: matches 16. .449 of consens: 27314. .27378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41105. .41405

/note="LIPA16 repeat: matches

complement(<41293. .41574)

/note="match: GSS AQ098779"

41865. .41922
                                                         /note="LIMC4 repeat: matches 5761.
53763. .53936
                                                                                                                                                                                                                                                                                                                                                                     /note="LIM2 repeat: matches -674. .654 of consensus"
complement(49576. .49922)
/note="match: z94578 chromosome 20 HindIII fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 repeat: matches 91. .2482 of consensus"
46916. .48259
                                                                                                                                                                                                                                            0799. .blz+v
/note="L1ME repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27391. .27432
/note="21 copies 2 mer tt 83% conserved"
27774. .27814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="L1M1 repeat: matches 1554..4497 of consensus"
19103..39247
inote="Alugo repeat: matches 1..210 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="L2 repeat: matches 2632.
27871. .28175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="L2 repeat: matches 2685. .2750 of consensus"
                                    'note="MER5B repeat:
                                                                                                           note="L1ME repeat:
                                                                                                                                                                   note="MER58A repeat: matches 2.
31774. .52319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluY repeat: matches 1.
3891. .43903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 91.
                                                                                                                                                note="L1ME repeat: matches 4567.
                                                                                                                                                                                                                                                                                                                                 note="LIMEc repeat: matches 1728. .1978 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"L1M3c repeat: matches 1470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"AluJb repeat: matches 2.
                                                                                                                                                                                                                       te-"L1ME repeat: matches 4323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  te="L1MA4A repeat: matches 84...45092
                                                                                                                                                                                                                                                                                              e="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="L1 repeat: matches 3000. .3011 of consensus"
)4. .44683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="AluJo repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="L1 repeat: matches 2583. .3000 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="LlMA10 repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2. .30623
e="Alusg repeat: matches 4.
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e="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2. .32141
e-"Alusx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 4177. .6146 of consensus
repeat:
                                                                                                             matches 5281.
                                                                                                                                                                                                                                                             matches 3855.
                                    matches 13. .177 of consensus"
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matches
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247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .149 of consensus"
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                                                                                                                                                                                    .224 of consensus"
                                                                                                             .5436
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                                                                                                                                                .5129 of consensus"
                                                                                                                                                                                                                         .4567 of consensus"
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. 387
                                                                         .5924 of consensus'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i (bases 1 to 3105)
Garnier,T. and Cole,S.T.
Characterization of a bacteriocinogenic plasmid fr
perfringens and molecular genetic analysis of the
bacteriocin-encoding gene
J. Bacteriol. 168 (3), 1189-1196 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M14481.1 GI:150736
bacteriocin; bacteriocin BCN5.
Plasmid pIP404 (clone: pT915.) DNA.
Plasmid pIP404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Draft entry and computer-readable sequence of [1] kindly provided by S.T.Cole ,10-FEB-1987.

A region of dyad symetry (21 bp inverted repeats with 5 bp in between) is found at positions 2973-3019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIP404BCN 3105 bp
Plasmid pIP404 (from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete cds.
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/product="bacteriocin"
/product="bacteriocin"
/proteain_id="aaa98248.1"
/db_xref="pid:g150737"
/db_xref="pid:g150737"
/db_xref="g1:150737"
/db_xref="g1:150737"
/db_xref="sid:g150737"
/db_xref="g1:150737"
/db_xref="sid:sneknivlvoyprissgrrogyvrnatslikykddyswygsfpg
RTVSDGDEITVLFISNEKNIVLLVOYPTSSGYROGYVTNATSLIKYKDDYSWYNGSTPE
PYDFDKTTQ1GTLDPRERAVVLYKVDGMTYVAXDTGKGKLTKSGLVHYEGSSSTGG
GSFNGVAPGEVVPGGFTYENNAEVVGDELYLRDANGNILTGRSVSVGDKITVLDVGYT
KQLALVOYPAGDVVROGYVTNATNLIRFNQYSWHNGSTSEEVLDENGGHLGSLNPYE
AATLLYEKNGMKHYVYDTNKGPWTKSGYVKYEGAATRVDIPYESITNAQKIVYGLSG
RGRELAAYKVGNGSNSLVFVCA.HGWEDNWAADGIELTRIGNGLIEHFQNAGTNWSL
YIIPVANPDGLSEGFTNNGPGRCTIVGAVCNAEPLGFSPGGVBFYHSGSEPLSVS
SKSLHDFIGGVKNRTSGEMCVIDLHGWEGAAIGNPEIGSYFRNOFGGORSGSONRG
FMIGWAKSIGAKAALLELPGSTKSHSDVVNGRYLQKIINAVTNLIGGSGGSSSGGSSF
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/note="L1MB7 r
55299. .55460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"LTR16C repeat: matches 70. 55709 .55812 /note-"MER14 repeat: matches 6... 55771 .55962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER34 repeat: 56696. .56839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Plasmid pIP404"
/plasmid="Plasmid pIP404"
/specific_host="CPN50"
/db_xref="taxon:2573"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"LTR29
                                                                                                                                                                                                                                                                                                                                   /gene="bcn5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 clone="pT915."
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                                                                                                                                                                                                                                                                                                                                                                         bcn5
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Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens plasmid 19 (2), 134-150 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 775 to 1224; 7031 to Garnier, T. and Cole, S.T. Studies of UV-inducible promote
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Plasmid pIP404 (from
M32882 J03309 J03310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Draft entry and computer-readable sequence for [1],[2] kindly submitted by T.Garnier, 15-DEC-1988.
Location/Qualifiers
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Plasmid pIP404
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upstream of HindIII site.
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89.5%;
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Pred. No. 82;
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KDLDMSDENIYITLNTFYKPCRRLENIKELNTLFIDLDYYKTGKTKDQVLMDLEKNYF

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misc_feature
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5514...5870
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|oin(8217. .10206,1. .855)
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ACCESSION
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Sutton,G.G., Blake,J.A., FitzGerald,L.M., Clayton,R.A.,
Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,M.D.,
Reich,C.I., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,
Merrick,J.M., Glodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F.,
Fuhrman,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,
Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,
Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,
Roberts,K.M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M.,
Smith,H.O., Woese,C.R. and Venter,J.C.
Complete genome sequence of the methanogenic archaeon,
Methanococcus jannaschii
Science 273 (5278), 1058-1073 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bult, C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D., Sutton, G.G., Blake, J.A., Fitzcerald, L.M., Clayton, R.A., Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J., Adams, M.D. Reich, C.I., Overbeek, R., Kirkness, E.F., Weinstock, K.G., Merrick, J.M., Glodek, A., Scott, J.D., Geoghagen, N.S., Weidman, J.F. Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Kelley, J.M., Peterson, J.D., Saddow, P.M., Hanna, M.C., Cotton, M.D., Hurst, M.A., Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (27-AUG-1996) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
On Jan 30, 1998 this sequence version replaced g1:1591213.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschil section 43 of 150 of the complete U67501 L77117 g2826289
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                                                                                                                                                                                                                                                                                                                                                                                     complement(869. .1537)
/gene="MJ0511"
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/translation="MLCIKKPSVASAFNELIPKILKDGEVVETEFEERTKEIRNTIIE
ITHEKLKKVPEKYPLGEKAVEEYTKNLLYGSKNVFSYDYHQRLFEYPYADEKINQIDY
IIEKLNQQKNSRRAVAITWNPKIDIEVSRDERGSVPCLQLVQFLIRNGKLYQTVIFRS
                                                                                                                                                             /product="thymidylate synthase (thya)"
/protein_id="AAB98502.1"
/db_xref="pID:g_591214"
                                                                                                                                                                                                                                                                                                                                     complement(869. .1537)
/gene="MJ0511"
complement(1875. .2588)
                                             NDALLAFVSNAIGLITLGEYIAKKVGVGYGTYTHHAISMHIYVDRDFDYIKKYFPECL
                                                                                                                                                                                                                                                                                   /note="similar to GP:1103708 percent identity: 39.38; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Methanococcus
/db_xref="taxon:2190"
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/note="similar to GB:J04540 PID:149734 GB:AE000666 percent identity: 41.49; identified by sequence similarity; putative"
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putative"
                                                                                                                                                                                                                       /translation="MIKEIIAKHFNLADKNIQLLPKFNIILNKREIIVKEDKCISCGK
CIEICPVNAITYSSDGLYITINKEKCVFCGKCKKVCPTNAIVIIRLRCEINEDARIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:M34016 PID:149806 percent identity: 37.04; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4517. .5008)
/gene="MJ0514.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MJ0514.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDKVKINKDKCILCGRCVDVCPTNAIKMWEKK"
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TKCIRCNLCYKECPUAIEKAKVKKSAKIIEDKCVKCEICAQTCFVGAIYVIEGRAEI
EDSEVHYTIKEKSIPHRKIRLKKYELDENTCIKCGICARFCPTNAIKAVRRKSIEVL
DLCMGCGACAEVCPKKCIKVERELGEVIKTRDIEVDKNLCVGCLVCIEECPINAIDQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3721. .4473)
/gene="MJ0514"
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/transi_table=11
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/protein_id="Asb98512.1"
/db_xref="PID:g1591216"
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/gene="MJ0513"
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                                                                                      complement(4986.
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                                                                                                                                                                                                VDKYEFIDYISERCASCLVCLRNCPFNAIEEYGSKIRIDINKCELCGKCEEICPLNAI
                                                                                                                                                                                                                                                                                                     /product="polyferredoxin
/protein_id="AAB98510.1"
/db_xref="PID:92826292"
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ITYLDINGYPIQRGIIYGIYYGYQHKRTSTGKDYTIFRIFDGYGWGRLRLFGIKANPE
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                                                      /gene="MJ0514.2"
                                                                                                             /gene="MJ0514
                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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'note="similar to GB:AE000666 percent identity: 37.01;
Identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                    /db_xref-"GI:2826292"
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17; Conserv
                                                             Conservative
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/translation="MSSAWATIPIGPIHPVLKEPLRIKLVLDGEKPVDAEIEMGYVHR
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DINREMMDEIYKKLDIFEDELKNIIEWFETGPLLALRSKEIGTILFYHEWARTRAVGPIR
DINREMMDEIYKKLDIFEDELKNIIEWFETGPLIALRSKEIGTILFYHEWARTRAVGPR
ERGSGLEESDWRLRHSTYGELKEKFVWREEGGNFARMAVRHEBIIESVRLIREALEHY
EECSGDIRVKAEIKGGKGEWRNEAPRGEVTYRMEITDGGIIKRIMIRTFTVMNLEAYK
YMLKTCFTVADAVSAYTSIDPCYSCTERCIVAVKDGKEIPISIKFR"

complement(7344. 7790)
/gene="MJ0516"

complement(7344. 7790)
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/protein_id="AAB98506.1"
/db_xref="FDI:gl591220"
/db_xref="GI:1591220"
/db_xref="MVIMTEIVIDKKYVENSLKQKMNVLKDNRFLMDDVFIPIAKAL
KITVEEVIEITAKKLDFASCYELHAYAEQAKMGCLGRKVDIDLGLCWLSDFFGLIKKE
EADLIRKKVVESYLLYKKPYKEALEEGRQMIIKLLKEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7904..8326)
/gene="MJ0517"
complement(7904..8326)
/gene="MJ0517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MMKELFRKRSIHVCVVNTGGCNGCDIEIVACLAPRYDIEQYGIY
VHNNPREADVLLVTGPVTLQWAERLKEIYEKTPEPKIVVAVGACALSGGIFKEGHVVG
GVDKVIPVDAKIPGCPPRPSEIIETILKVAPKAIAMREKRLKNKDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="carbon monoxide dehydrogenase, hydrogenase
subunit CooH (cooH)"
/prottein_id="Ass98504.1"
/db_xref="PID:g1591218"
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complement(6209. .7351)
/gene="MJ0515"
/gene="MJ0515"
/note="similar to GP:1498746 percent identity:
identified by sequence similarity; putative"
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EMDKHRVETEGLFEDKPKYSNLIIDEEVCVRCGNCERACPINVIERKEGKYVINMAL
GISCKECIKVCPIENATVVVDEKTLKEKIDKAFEIKNKKITGKLEIKENVIEKIPHIVS
GLCVSCGICKDVCVGEIDLNEKKVVECVKCGLCIEVCSTTAIRIYKPIIPKRKDICYV
IDEDLCIGCRICQKVCGSGAIKISKETKLPYIVPELCVRGGACARECPVGAIKVVKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subunit CooL (cooL)*
/protein_id="AAB98505.1"
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identified by sequence similarity; putative"
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                                                                                                                                                                                                   complement(8320.
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identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:2826290"
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/db_xref="PID:g2826290"
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                                                                                       83.2%;
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                                                          Score 15:8; D
Pred. No. 83;
0; Mismatches
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JOURNAL MEDLINE REFERENCE AUTHORS
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CSU23186/c
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U23186
                                                                         sequence.
295331
295331.1 GI:2281936
HTG; Brain Protein E46-like; CpG island; FBLN1; FIBULIN-1 ISOFORM
PRECURSOR; FIBULIN-1 ISOFORM C PRECURSOR; FIBULIN-1 ISOFORM D
                                                                                                      HS941F9 127583 bp
Human DNA sequence from
Contains ESTs, STSs and
part of a Brain Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (21-MAR-1995) Ted R. John, Molecular Biology, Univ. of Wyoming, Box 3944 University Station, Laramie, WY 82071-3944, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   John, T.R., Smith, J.J. and Kaiser, I.I. A phospholipase A2-like pseudogene retaining the highly conserved introns of Mojave toxin and other snake venom group II PLA2s, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mojave rattlesnake. Crotalus scutulatus
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/gene="psi-Mtx"
a 660 c 624
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2133. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Crotalus scutulatus"
/sub_species="scutulatus"
/db_xref="taxon:8737"
525, ..530
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/gene="psi-mtx"

join(557. 573,648. 798,966. 1098,1574. 1674,1934. 2158)

/gene="psi-mtx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exist in reality,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PLA2-like protein; This protein probably
exist in reality, but only as an ORF on a pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(<974. .1098,1574. .1674,1934. .2076)
/gene="psi_Mtx"
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Pred. No. 82;
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                                                                                               DNA PRI 28-MAY-1998
BAC 941F9 on chromosome 22q11.2-qter.
3' part of FIBULIN-1 D PRECURSOR like gene,
E46 like gene and a CpG island, complete
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On Jul 28, 1997 this sequence version replaced gi:2094794.

IMPORTNANT: This sequence is the entire insert of clone 941F9. This
sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre chromosome 22
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22/
This sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The true left end of clone 941F9 is at 1 in this sequence. The true left end of clone N38E2 is at 9038.

The true right end of clone N38E2 is at 54042.

The true left end of clone 398C2 is at 87881.

The true right end of clone 941F9 is at 127583.

941F9 is from the human BAC library described in U-J. Kim et al. (1996) Genomics 34, 213-218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 127583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-JUL-1997) E-mail enquires: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                           /note="MIR repeat: matches 73. .141 of consensus"
10365. .10818
/note="match: multiple ESTs; match: C18390 H02670 R23566
R25317; match: R68138 R24691 R78762 T39562; match: R76275
R62365 T49888 R68191; match: F16897 C02271 R23566; similate of F180LIN-1 ISOFORM C PRECURSOR"
                                                                                                                                                                                                                                                                                                                                                                                                    y139. .9576
/note="MLT2B repeat:
9520. .9844
                                                                                                                                                                                                                                                                                                                                                              9520. .9844
/note="match: 5' ESTs C16630, C16762 -
9777. .9850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3451. .3752
/note="AluSx repeat: matches 302. .1 of consensus"
3753. .9137
                                           /note="MIR2 repeat: matches 4. .146 of consensus"
12336. .12815
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MLT2_internal repeat: matches 5383. .2 of consensus"
9139. .9576
                                                                                     /note="MIR repeat: matches 120.
12134. .12269
                                                                                                                               /note="MIR repeat: matches 144. .109 of consensus" 11526. .11571
                                                                                                                                                                        /note="match: STS R76273" 11113. .11148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3169. .3420
/note="MLT2_internal repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus"
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/db_xref="taxon:9606"
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note-"match: multiple ESTs; match: R33281 H02060 R78704; imilar to FIBULIN-1 ISOFORM B PRECURSOR"
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21967. .>48546
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/note="match:
13033. .13136
                                                                                                                                                                                                                                                                                                                                                      /note="match: multiple ESTs; match: R21642 W46777 H45729 W56058 R68369; match: R76745 H39633 H13045 N76544 H29751; Watch: W86968 N57451 H55328 W95973 R74257; match: H29751 W46339 H02394 W95130 T49630; match: W32387 W76015; similato FIBULIN-1 ISOFORM D PRECURSOR"

join(<21967. 22109,24433. .24564,47763. .47902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR2 repeat: 21967. 47000
                                       /note="Alux repeat
22733. .22735
/gene="bK941F9.1"
                                                                                                                        /translation="LQQEKTDTVRCIKSCRPNDVTCVFDPVHTISHTVISLPTFREFT
RPEEIIFLRAITPPHPASQANIIFDITEGNLRDSFDIIKRYMDGMTVGVVRQVRPIVG
PFHAVLKLEMNYVVGGVVSHRNVVNVHIFVSEYWF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSg repeat:
17129. .17326
  /note="clone cN38E2;
/replace="cca"
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/protein_id="CAB08593.1"
/db_xref="pID:e128B141"
/db_xref="pID:93087786"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MER42c repeat: matches 296. .549 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MLT1B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="2 copies of 57 mer 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="3 copies of 57 
|6027. .16197
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(3237. .13535
                                                                                                                                                                                          'db_xref="SPTREMBL:060822"
                                                                                                                                                                                                                                                                                                                                      'gene="bK941F9.1"
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.8687. .18792
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Direct Submission
Submitted (09-JUN-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 6, 1999 this sequence version replaced gi:4680418.
                                                                                                                                                            HTG;
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 156791)
                                                                                                                                                                                                                                 Human DNA
                                                                                                                                                                                                                  sequence
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                                                                         Matthews, L.
                                                                                                                                Homo sapiens
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24154 . 2420
/note="MIR repeat: matches 61.
25946 . 26009
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/note="2 copies of 32 mer 91 % conserved"
/16606. .36689
/note="MIR repeat: matches 206. .106 of consensus"
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40235. .40237
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="7 copies of 37 mer 99 % conserved" 39781. .40083
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/replace="acg"
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/note="16 copies of 2 mer 84 % conserved"

31244. 31279
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/replace="agc"
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/replace="cga"
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34691. .34918
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/replace="cac"
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'note="3 copies of 16
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone 860P4. This sequence has been finished according to sequence map criteria as follows. Attempt 1s made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr20
860P4 is from the library RPCI5 constructed at the Roswell Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was generated from part of bacterial clone contigs human chromosome 20, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer Institute by the group of Pieter de Jong. For furthed details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature key
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/note="11 co
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'Note-"7 copies 5 mer gggag 86% conserved"

3081. 3480

'note-"Charlie4a repeat: matches 20. .447 of consensus"
                             11482.
                                                                                                                                           /note="AluSg/x repeat: matches 158.
10424. .11188
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                             'note="AluSgl repeat: matches 1. .297 of consensus"
11482. .12592
                                                                                                             'note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MLT1F repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="308
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/note-"Alujb repeat: matches l.
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                                                                                                                                                                                                                              'note="L1MEc
                                                                                                                                                                                                                                                                                    'note-"MER1B repeat:
                                                                                                                                                                                                                                                                                                                                               'note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                  0866. .9399
Onote="LIMEC repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="L2 repeat: matches 2611. .2730 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 5303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copies 2 mer tt 62% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copies 18 mer 69% conserved"
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repeat: matches 2569.
                                                                                                                                                                                                                           repeat:
                                                                                                                                                                                                                                                                                                                                                                                                     matches 702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 16. .532 of consensus"
                                                                                                                                                                                                                              matches 1475.
                                                                                                                                                                                                                                                                                    matches 1. .336 of consensus"
                                                                                                                                                                                                                                                                                                                                               matches 1293.
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                                                                                                                                                                                                                                                                                                                                                                                                        .1255 of consensus"
.3716 of consensus"
                                                                                                                                                                                                                           .1773 of consensus
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                                                                                                                                                                   .306 of consensus"
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/note="MLTIG repeat: matches 51. .512 of consensus"
32067. .32272
/note="MIR repeat: matches 12. .235 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27653 .27740

/note="22 copies 4 mer ggaa 91% conserved"
28338 .28417

/note="MIR repeat: matches 67. .150 of consensus"
28480 .28535

/note="14 copies 4 mer gatg 88% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23451. 24088
/note="LTR9 repeat: matches 12..625 of consensus"
25150. 25237
/note="MIR repeat: matches 27..123 of consensus"
25249. 25866
/note="AlluJb repeat: matches 1..305 of consensus"
27260. 27544
       /note="LTR16C repeat: matches 55.
40881. .41250
                                                                                                                 38035
                                                                                                                                                                                         /note="AluSx repeat: matches 1. .295 of consensus"
34129. .34244
                                                                                                                                                                                                                                                                                                                                                                                                              30559
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="4 copies 18 mer 78% conserved"
30312. .30564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="39 copies 2 mer ta 71% conserved" 30238. .30309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LiMC3 repeat: matches 6109. .7739 of consensus" 30176. .30213
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/note="5 copies 26 mer 68% conserved"
27566. .27737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1..309 of consensus" 27545..27606
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13628. .14345
/note="SVA repeat: matches 684. .1386 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SVA repeat: matches 3. 13349. .14389
                                           /note="MLT1G repeat: matches 13.
39958. .40252
                                                                                                                                                                                                                                                                                                                                                   30559. .30684
/note="7 copies 18 mer 71% conserved"
30694. .31030
/note="11MC4 repeat: matches 6026. .6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="LIME repeat: matches 5316. .5743 of consensus"
18943. 18976
/note="17 copies 2 mer ta 82% conserved"
19445. 19747
/note="AluSq repeat: matches 1. .313 of consensus"
20812. .20959
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/note="LIMC3 repeat: matches 6354. .6609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="31 copies 2 mer ga 79% conserved"
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                                                                             /note="AluSx repeat:
38876. .39322
                                                                                                                                /note="MLTIA2 repeat: matches 1.
                                                                                                                                                     /note="MSTB repeat: matches 307.
35029. .35403
                                                                                                                                                                                                                                       note="MSTB repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MADE1 repeat: matches 1. .38 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 137. .262 of consensus"
29025. .30142
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                                                                                                                                                                                                                                             matches 1.
                                                                                                                                                                                                                                                                                                                                                     matches 6026. .6136 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 25.
                                                                                              matches 42.
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                                                                                                                                                                                                                                             .307 of consensus"
                                                                                                                               .370 of consensus"
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1 (bases 1 to 87857)

Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.

Sequencing of human chromosome 5

Unpublished
3 (bases 1 to 87857)
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                        Unpublished
                                                                      Large Scale Sequence Analysis and Comparison Analysis (SCAN) System
                                                                                                             Ricke, D.O.
                                                                                                                             (bases 1 to 87857)
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/note="19 copies 18 m
48522. .48843
/note="161 copies 2 m
48549. .48838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48491. .48848
/note="Tandem repeat. Tandem repeat region, contains one forced join. Digest suggests there may be 700bp missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MLT1B repeat: matches 1.
41579. .41798
.note="HALL repeat: matches 141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER3 repeat: matches 68. .205 of consensus" 46958. .47061
/note="L1 repeat: matches 3628. .3731 of consensus" 47331 .47625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="5 copies 58 mer 718
48587. .48844
/note="6 copies 43 mer 638
48647. .48854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LIME3A repeat: matches 5594. .6117 of consensus"
44023. .44415
/note="MSTB repeat: matches 13. .426 of consensus"
46015. .46146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41841. .41908
/note="17 copies 4 mer gaag 91% conserved"
41927. .42194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41800. .41928
/note="3 copies 43 mer 76% conserved"
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42902. .43388
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2326. .42459
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Direct Submission
Submitted (31-0CT-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence submitted by:
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Location/Qualifiers
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complement(25131.
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BASE COUNT
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Qy 1 gatggattagcagagggtt 19 |||||||| |||||||| | Db 66996 GATGGATTGTCAGAGGGTT 67014

Gaps

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Search completed: August 18, 1999, 17:17:19 Job time: 3485 sec

44

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1496 7902

Q28119 V52245

P.falciparum LSA g Streptococcus pneu

# GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 1999, 17:18:31; Search time 148.09 Seconds (without alignments) 32.100 Million cell updates/sec

Title: Perfect score: US-09-004-395-4

Sequence: gatggattagcagagggtt 19

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database : N\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|              |            |        |          |                    |                    |          |        |                    | C     | •              |        |                     | •              | ٠.           | ი      |        |            |        | ი      |           |                    |                    |                    | C                  |           | 2 0         | · 0                | . 0         | n      | 0 0        | n          | Ω      | a                  | ი      | O      | a      |        |        |        |           |        | ი       | ი        | Resul<br>No    |
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| 74.7         | 74.7       | 74.7   | 74.7     | 74.7               | 75.8               | 75.8     | 7.9    |                    |       |                |        |                     | 0              |              |        | 77.9   | _          | 77.9   | 77.9   | _         | 7.9                | 7.9                |                    | ) <u> </u>         |           |             | , <u>-</u>         | . <u> </u>  |        |            |            |        | 1.1                | 1      | 1      | -      | 1      | 81.1   | 1.1    | 83.2      | 3.2    | 100.0   |          | Query<br>Match |
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| Q28115       | N92937     | N90733 | N90732   |                    | V21209_03          | Q61383   | X16323 | V21209_07          |       | VE0001         | 1450/4 | 100100              | 136100<br>1000 | 005025       | 095035 | 067390 | 044277     | Q44278 | Q37757 | Q38104    | Q38105             | 201809             | 003374             | V/2126             | V/211/    | X15925      | X15923             | V60321      | V60320 | 47.876     | V2/8/5     | V22428 | V22426             | V22382 | V22380 | V22379 | Q90982 | Q90972 | Q62461 | V21209_10 | Q80916 |         | 2        | ij             |
| ciparum LSA- | om Plasmod |        |          | Malaria-specific P | Continuation (4 of | ain E    | g      | Continuation (8 of | שי    | uman Binl gene |        | nullan gene signatu | ۰              | h topocumput |        | Z.     | erglycin - | 5      | •      | PHEBO-DR- | Vector phebo-DR-LU | Consensus sequence | Partial sequence o | Human catalytic te | catalytic | otide seque | cDNA encoding a ca | natively sp | ase    | telomerase | telomerase |        | Human telomerase r |        |        |        | p140   |        |        | 5         | falcip | (3<br>0 | n (2     | Description    |

RESULT
Q80916
ID Q80916
AC Q88
AC Q8
DT 29
DT 29
DT P1
KW mu
KW ma
KW ma
CS P1
PN WCC
PD 22
PT 1C

D 080916 standard; cDNA; 1320 BP.
C 080916;
C 080916;
Y 29-AUG-1995 (first entry)
Plasmodium falciparum LSA-1 repeatless gene; recombinant poy
multicomponent multistage malarial vaccines; immunogens;
W mularia diagnosis; ss.
Plasmodium falciparum (pLSARPLS.I4L.1).

recombinant poxvirus;

Ş 밁

Query Match 100.0%; Score 19; DB 1; Length 110000; Best Local Similarity 100.0%; Pred. No. 0.97; Matches 19; Conservative 0; Mismatches 0; Indels 0;

Gaps

| Query Match Query Match Query Match Query Match Query Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 gatggattagcagaggtt 19 Qy 1 liiiiiiiiiiiiiii Qb 105074 GATGGATTAGCAGAGGGTT 105056 | RESULT 1  X20248_01/c Continuation (2 of 10) of x20248 from base 100001 (Borrelia burgdorferi p Wp Sequence split into 10 fragments nccus x20248 Accession x20248 Wp X20248_01 110000 Wp X20248_01 100001 210000 Wp X20248_02 200001 310000 Wp X20248_03 300001 410000 Wp X20248_04 400001 510000 Wp X20248_05 500001 510000 Wp X20248_05 600001 710000 Wp X20248_06 600001 710000 Wp X20248_07 700001 810000 Wp X20248_08 800001 910715 | ALIGNMENTS     |
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|                                                                                                                                                                                                      | Query Match 100.0%; Score 19; DB 1; Length 110000; Best Local Similarity 100.0%; Pred. No. 0.97; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 1 gatggattagcagagggtt 19 1                                                                                                                                                                                                                                                     | ## SULT 1    1 |

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RESULT 4
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RESULT
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Matches 17
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Best Local Similarity
Matches 17; Conser
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                  Q62461;
09-NOV-1994 (first entry)
Human embryonal kinase 2 receptor.
Embryonal kinase; HEK; protein tyrosine kinase; PTK; tumour;
cancer; therapy; amplification; primer; polymerase chain reaction;
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(VIRO-) VIROGENETICS CORP.
De Taisne C, Paoletti E,
WPI; 95-036113/05.
                                                                                                                          Q62461 standard;
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17; Conser
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17 fragment
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Pred. No. 39;
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RESULT Q90982

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Sc Claim 5; Page 25-27; 42pp; English.

A CDNA library was established from rat skeletal myoblast cell line L6. DNA fragments of approx. 400 bp were recovered and subjected to cloning. 20 plasmids were sequenced. Sequence data of cDNA fragments were constructed to the linkage sequences with the DNA programme DNASIS. The basic sequence protrayed in 090972 was hence constructed. From sequence data of the whole cDNA length, the ORF was determined. The AA sequence was further translated and the sequence thus established is illustrated in R75843. One of the frames possesses the 2993-bp ORF, that was approximated to 3000 bp of the whole ORF length of the Eck family.

Sequence 4027 BP; 885 A; 1141 C; 1166 G; 835 T;
                                                  Query Match
Best Local S
Matches 16
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Best Local Similarity 94.1
Matches 16; Conservative
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Claim 4; Page 7-10; Ilpp; German.
Claim 4; Page 7-10; Ilpp; German.
RNA from human embryonic tissue was isolated.
primer P6(4) PTK-specific cDNA was synthesised.
primer B6(4) and N5. A 2097 by
amplified using primers P6(4) and R5. A 2097 by
obtained. Primers E3, P12 and E6 were the
c-terminal of the HEKZ receptor gene.
Sequence 3751 BP; 739 A; 1150 C; 112:
3433
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14-APR-1994.
07-OCT-1992; 233782.
07-CCT-1992; DE-233782.
(CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
                                                                                                                                                                                                                                                                                                   WPI; 95-226291/30.
                                                                                                                                                                                                                                                                                                                                           28-JUN-1995.
24-NOV-1994; 118524.
24-NOV-1993; JP-3158
                                                                                                                                                                                                                                                                                                                                                                                 Rattus rattus.
EP-659883-A.
                                                                                                                                                                                                                                                                                                                                                                                                        Protein p140;
Protein p140;
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                                                                                                                                                                                                                                                                                                               (ONOY ) ONO PHARM CO LTD.
Kitagawa K, Ohno H, Taj
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q90972 standard;
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                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         cDNA from insulin;
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94.1%;
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94.1%;
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3449
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Pred. No. 45;
0; Mismatches
                                                  Score 15.4; Depred. No. 45; O; Mismatches
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Best Loc
Matches
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Kitagawa K, Ohno H,
WPI; 95-226291/30.
P-PSDB; R75844.
                                                                                                                                                                                                                                                           0B2317891-A.
0B-APR-1998;
01-OCT-1997;
11-AUG-1997;
11-APR-1997;
18-APR-1997;
25-APR-1997;
06-MAY-1997;
14-AUG-1997;
14-AUG-1997;
                                                                                                                                                                                                                        (GERO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
Protein
                  cell proliferation conditions especially cancer and ageing Claim 5; Fig 16; 387pp; English.
The present sequence encodes human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also
                                                                           Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
                                                                                                                                                         (UYTE-) UNIV TECHNOLOGY CORP. Andrews WH, Cech TR, Chapman Morin GB, Nakamura T, Harley WPI; 98-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human telomerase reverse transcriptase encoding cDNA.
Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
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24-NOV-1993;
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28-JUN-1995.
                                                                                                                                          P-PSDB; W46957
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US-915503.

US-724643.

US-844419.

US-846017.

US-851843.

US-851843.

US-91313.

US-91313.2.
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JP-315806
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  is a ribonucleoprotein. following methods: (A) of
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rom rat skeletal muscle myoblast cell line L6.
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Pred. No. 4
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Best Loc
Matches
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                                                                                                                                                         Pure and recombinant human Telomerase Reverse Tran variants - are useful in the diagnosis, prognosis cell proliferation conditions especially cancer an Example 1; Fig 18; 387pp; English
                                                                                                                                                                                                                        Morin GB, Nakamura
WPI; 98-171633/16.
P-PSDB; W46998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human telomerase reverse transcriptase cDNA clone 712562.
Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
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Pred. No. 45;
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V22382/c
ID V22382 standard; cDNA; 3855
AC V22382;
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            Disclosure; Fig 20; 387pp; English.

The present sequence encodes a human telomerase reverse transcriptase (hTRT) variant from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein of preparation of hTRT with a telomerase by contacting a protein of preparation of hTRT with a telomerase NNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) concreasing the proliferation of a vertebrate cell by increase in cell vertebrate cell proliferation to create a medicament that inhibits agent has a protein preparation of hTRT and the polynucleotide encoding the prosence of in the sample; and the proliferation of a protein that inhibits are the manufacture of hTRT and the polynucleotide encoding the presence of hTRT in the sample that inhibits are the manufacture of manufacture in the sample that inhibits are the manufacture of manufacture in the sample that inhibits are the manufacture of manufacture in the sample that inhibits are the manufacture of manufacture in the sample that inhibits are the manufacture of manufacture in the sample that inhibits are the manufacture of manufacture in the sample that inhibits are the manufacture of manufacture in the sample in the sa
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Matches 16
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08-APR-1998.
01-OCT-1997; US-915503.
14-AUG-1997; US-915503.
10-OCT-1996; US-724643.
18-APR-1997; US-844419.
25-APR-1997; US-8446017.
06-MAY-1997; US-851843.
09-MAY-1997; US-851843.
09-MAY-1997; US-9131312.
14-AUG-1997; US-9131312.
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Andrews WH, Cech TR, Chapman KB, Harley C, Lingner Morin GB, Nakamura T, Harley CB;
WPI; 98-171633/16.
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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
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94.18;
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RESULT 11
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    PT Pure and recombinant human Telomerase Reverse Transcriptase and its PT variants - are useful in the diagnosis, prognosis and treatment of PT cell proliferation conditions especially cancer and ageing PS Example 1; Fig 68; 387pp; English.

CC The present sequence represents a human telomerase reverse transcriptase CC (hTRT) DNA clone from the present invention. The present invention also describes the following methods: (A) determining whether a test compound CC is a modulator of hTRT, by detecting the change in hTRT recombinant CC protein or polynucleotide, on administration of the compound; (B) preparation of frecombinant telomerase by contacting a protein of CC the hTRT RNA or protein in a sample by binding a relevant probe to the CC sample and detecting the complex formed or in the case of RNA detection, CC amplifying the product with presence of hTRT in the sample; and (D) CC increasing the proliferation of a vertebrate cell by increasing hTRT CC expression; and (E) the use of an agent that causes an increase in cell cell vertebrate cell proliferation to create a medicament that inhibits CC ageing. A protein preparation of hTRT and the polynucleotide encoding the fact of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase call conditions that are associated with high telomerase conditions that are associated with high telomerase activity can be used in the manufacture of hTRT can also be used in the new call conditions that are associated with high telomerase call call the new call conditions that are associated with high telomerase call call the new call call the proliferation of hTRT can also be used in the new call call the polynucleotide encoding the call call the proliferation of hTRT can also be used in the new call call the polynucleotide encoding the call call the proliferation of the call call the polynucleotide encoding the call call the proliferation of the call call the new call call the proliferation of the call call th
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Matches 16
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06-MAY-1997; US-851843.

09-MAY-1997; US-854050.

14-AUG-1997; US-911312.

14-AUG-1997; US-912951.
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08-APR-1998.
01-OCT-1997;
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(GETE-) MINV TECHNOLOGY CORP.
ANDREWS WH, Cech TR, Chapman
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01-OCT-1996; US-724643.
18-APR-1997; US-844419.
25-APR-1997; US-846017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morin GB, Nakamura
WPI; 98-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prognosis; cell proliferation;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human telomerase reverse transcriptase 63 kDa clone 712562.
Human; telomerase reverse transcriptase; hTRT; TRT; diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V22426;
13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W56109
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/transl_except= (pos:325. .327,aa:xaa)
/note= "Xaa= unspecified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.1%;
94.1%;
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Pred. No. 45;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harley C, Lingner
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RESULT 1
V22428/c
                                                                               PT Pure and recombinant human Telomerase Reverse Transcriptase and its PT variants - are useful in the diagnosis, prognosis and treatment of PT cell proliferation conditions especially cancer and ageing Example 1; Fig 74; 387pp; English.

CC The present sequence encodes human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant CC protein or polynucleotide, on administration of the compound; (B) protein or polynucleotide, on administration of the compound; (B) preparation of hTRT with a telomerase by contacting a protein of the hTRT RNA or protein in a sample by binding a relevant probe to the Sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or increasing the proliferation of a vertebrate cell by increasing hTRT CC expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding the used to treat conditions that are associated with high telomerase activity can be used to treat conditions that are associated with high telomerase.
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Best Local Similarity
Matches 16; Conserv
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Best Local
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01-OCT-1997; 020890.

14-AUG-1997; US-915503.

01-OCT-1996; US-724643.

10-OCT-1996; US-844419.

25-APR-1997; US-846017.

06-MAY-1997; US-851843.

09-MAY-1997; US-851843.

09-MAY-1997; US-911312.

14-AUG-1997; US-911312.

14-AUG-1997; US-911312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human telomerase reverse transcriptase encoding cDNA refined sequence Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; ss.
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Andrews WH, Cech TR, Chapman
Morin GB, Nakamura T, Harley
                                                                                                            activity. A protein
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P-PSDB; W56113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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                                                                                86
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/note= "refined sequence"
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                                                                                                            preparation
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94.1%;
                81.18;
94.18;
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Pred. No. 42;
0; Mismatches
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                Score 15.4;
Pred. No. 45;
 Mismatches
                                                                                                              of hTRT can
                                                                               1362
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cc in a cell is used to increase telomerase activity and thus careful is used to increase telomerase activity and thus careful is used to increase telomerase activity and thus careful disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to decrease telomerase cc activity, e.g. for treatment of cancer. TR2 polypeptides can also cc binding to TRIP1 (see W61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful cc in immunoassays and therapeutically as inhibitors. Nucleic acid cc fragments are used as diagnostic probes for detecting/quantifying cr pr DNA. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from centineered cells or gene therapy vectors.

Sequence 949 BP; 176 A; 331 C; 268 G; 174 T;
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Homo sapiens.
Key
CDS
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Example 5; Fig 7; 150pp; English.

Partial cDNA clone TP2-15 comprises the 3' region of human partial cDNA clone TP2-15 comprises the 3' region of human telomerase protein 2 (TP2) cDNA, 133 bases of which overlap with the 3' end of another partial clone, #32 (see V27872). It was isolated from a human colon tumour cell line LIM1863 cDNA library using an 830 bp XhoI fragment of clone #32 as probe. Clones TP2-15 and #32 have been combined to provide a full-length sequence (see Y27876) coding for human TP2 (see W61350). Expressing TP2 genes in a cell is used to increase the comprise activity and the sequence in a cell is used to increase the comprise activity.
                                                            12-OCT-1998 (first entry)
Human telomerase protein 2 (TP2) full-length cDNA
TP2; human; telomerase protein 2; cancer; AIDS; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
Harrington LA, Robinson MO;
WPI; 98-297946/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1998 (first entry)
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16-OCT-1997; US-951733.
15-NOV-1996; US-871189.
11-JUN-1997; US-873039.
                                                                                                                                        V27876 standard; cDNA; 3798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN CANADA INC.
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                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                  Conservative
 Location/Qualifiers
2. .3466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                    81.18;
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                                                                                                                                                                                                                                                                                                                                     Score 15.4;
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                   cancer; AIDS; ageing; therapy;
                                                                                                                                                                                                                                                                                                                      39;
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CT This full-length cDNA clone codes for a human telomerase protein C2 (TP2, see #61350), a novel protein of the telomerase complex. CC The sequence was deduced from overlapping partial clones #32 (see C2 (TP2), see Well350), which were obtained from a human colon tumour cell line LIM1863 cDNA. Expressing TP2 genes in a CC cell is used to increase telomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TR2 polypeptides can also be used to screen to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TR2 polypeptides can also be used to screen for agents that inhibit TP2 activity or its binding to TRIP1 (see W61347) or telomerase RNA, potentially useful therapeutically, c.g. for also to raise specific antibodies useful in immunoassays and therapeutically as inhibitors. Nucleic acid fragments are used cas diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered c.v., s.c. or orally, or they are delivered from engineered cells or gene therapy vectors.

Sequence 3798 BP; 613 A; 1311 C; 1212 G; 662 T;
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Best Local S
Matches 16
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22-MAY 1998.
13-NOV-1997; U21248.
16-OCT-1997; US-951733.
15-NOV-1996; US-871189.
11-JUN-1997; US-873039.
                                                                                 20-FEB-1998; U03404.
30-OCT-1997; US-064322.
20-FEB-1997; US-038750.
20-MAY-1997; US-047151.
01-AUG-1997; US-054549.
14-AUG-1997; US-055762.
(WHED.) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3205
                                                   Counter CM, Meyerson M, WPI; 98-495367/42.
                                                                                                                                                                                                                                                                                                     Human telomerase gene referred to as hEST2. Catalytic subunit; human; telomerase; telom diagnosis; treatment; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN CANADA INC.
(AMGE-) AMGEN INC.
Harrington LA, Robinson M
WPI; 98-297946/26.
                                                                                                                                                                                                      WO9837181-A2.
27-AUG-1998.
                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                        V60320;
04-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding human telomerase protein-2 - used for regulating telomerase activity, e.g. for treating cancer or acquired
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                    New isolated
                                       P-PSDB; W71376.
                                                                                                                                                                                                                                                                                                                                                                                     760320 standard; cDNA; 4023 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gatggattagcagaggg 17
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05 GATGGAGTAGCAGAGGG 31
                                                                                                                                                                                                                                                                                        sapiens
                    human
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613 A;
                                                                                                                                                                                                                                    Location/Qualifiers 59. .3458 /*tag= a
     for
telomerase catalytic sub-unit gene - used or increasing or reducing the life span of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.1%;
94.1%;
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                                                                 Weinberg
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Pred. No. 4
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such as cancer cells or transformed cells
Claim 5; Fig 5A-B; 96pp; English.
The present sequence encodes the catalytic subunit of a human
telomerase holoenzyme. Disruption of the telomerase gene alters
telomerase holoenzyme. Disruption of the telomerase activity,
and the protein is physically associated with telomerase and a
constituent of active telomerase complex. The products can be used
for increasing or reducing the lifespan of cells such as cancer cells
or transformed cells. They can also be used in the diagnosis and
treatment of mallynancies. In addition, cells with a longer lifespan
can be transplanted into or grafted onto an individual (e.g. as skin
grafts, as systems for delivery of therapeutic peroteins, such as hormones
and enzymes), to whom they provide therapeutic benefit.

Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T;
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                     Matches
                            Query Match
Best Local
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1 gatggattagcagaggg
                     16;
                     Conservative
                            81.18;
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                     Score 15.4; I
Pred. No. 45;
0; Mismatches
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Length 4023;

Search completed: August 18, 1999, 17:18:36 Job time: 3268 sec

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3196 GATGGAGTAGCAGAGGG

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19
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48.853 Million cell updates/sec
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Copyright (c) 1993 - 1998 Compugen Ltd.
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| 58:        | 57:        | 56:        | 55:        | 54:        |
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| em_est26:* | em_est25:* | em_est24:* | em_est23:* | em_est22:* |

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 1 16.4 86.3 371 21 T6427<br>2 16.4 86.3 374 24 R697<br>3 16.4 86.3 374 24 R697<br>4 16.4 86.3 379 33 AA393<br>5 15.8 83.2 309 24 H0144<br>6 15.8 83.2 309 24 H0144<br>6 15.8 83.2 309 24 H0144<br>6 15.4 81.1 407 20 T0933<br>7 15.4 81.1 267 22 R5046<br>11 15.4 81.1 267 22 R5046<br>11 15.4 81.1 367 30 AA241<br>15 15.4 81.1 303 31 AA299<br>15 15.4 81.1 303 31 AA299<br>17 15.4 81.1 303 31 AA299<br>18 15.4 81.1 303 31 AA399<br>18 15.4 81.1 303 31 AA399<br>19 15.4 81.1 428 37 AA683<br>11 15.4 81.1 428 37 AA683<br>11 15.4 81.1 403 42 A1153<br>20 15.4 81.1 403 42 A1153<br>21 15.4 81.1 403 42 A1153<br>22 15.4 81.1 403 42 A1153<br>23 15 78.9 520 20 A2671<br>24 16.8 77.9 320 24 A3067<br>27 14.8 77.9 320 27 AA0463<br>33 14.8 77.9 325 27 AA0463<br>34 14.8 77.9 325 27 AA0463<br>35 14.8 77.9 325 27 AA0463<br>36 14.8 77.9 325 32 AA350<br>37 14.8 77.9 325 32 AA350<br>38 14.8 77.9 355 32 AA350<br>39 14.8 77.9 355 33 AA442<br>40 14.8 77.9 333 33 AA442<br>41 14.8 77.9 563 33 AA442<br>42 14.8 77.9 563 33 AA442<br>43 14.8 77.9 563 33 AA442<br>44 14.8 77.9 563 33 AA442                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Result<br>No. | score | ner<br>mer | ength      | : DB     | B             |
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| 1 16.4 86.3 371 22 T59218 3 16.4 86.3 374 24 H61749 4 16.4 86.3 374 24 H61749 4 16.4 86.3 374 24 H61749 4 16.4 86.3 374 24 H61749 4 16.4 86.3 374 24 H61749 4 16.5 8 83.2 420 45 A13537 7 15.4 81.1 407 27 R50059 15.4 81.1 267 28 AA0990 15.4 81.1 16.2 30 AA2418 15.4 81.1 16.2 30 AA2418 15.4 81.1 342 30 AA2418 15.4 81.1 342 31 AA2990 15.4 81.1 379 34 AA4555 15.4 81.1 379 34 AA4555 15.4 81.1 379 34 AA4555 15.4 81.1 379 34 AA4555 15.4 81.1 379 34 AA4555 15.4 81.1 379 34 AA4555 15.4 81.1 4.8 37 AA683 17.9 528 47 A14857 78.9 502 31 AA3277 78.9 502 31 AA3277 78.9 502 31 AA3277 78.9 302 31 AA3277 79.9 302 | i             |       |            | 1 1        | : :      |               |
| 3 16.4 86.3 374 24 H61747<br>5 15.8 83.2 309 22 H01444<br>6 15.8 83.2 420 45 A13537<br>7 15.4 81.1 407 20 T79332<br>8 15.4 81.1 461 22 R50052<br>10 15.4 81.1 267 22 RA00902<br>11 15.4 81.1 267 28 AA0902<br>12 15.4 81.1 342 30 AA2418<br>13 15.4 81.1 342 30 AA2618<br>15 15.4 81.1 342 31 AA2908<br>16 15.4 81.1 303 31 AA2908<br>17 15.4 81.1 303 31 AA2908<br>18 15.4 81.1 303 31 AA2908<br>19 15.4 81.1 485 37 AA6838<br>19 15.4 81.1 485 37 AA6838<br>10 15.4 81.1 485 37 AA6838<br>10 15.4 81.1 403 42 A11533<br>11 10 10 10 10 10 10 10 10 10 10 10 10 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |               | თ თ   | οò         | 9 ~        | 22<br>22 | 901           |
| 4 16.4 86.3 239 23 AA3937 6 15.8 83.2 309 22 AF AF AF AF AF AF AF AF AF AF AF AF AF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |               | 6.    | 6          | 7          | 24       | 174           |
| 5 15.8 83.2 209 24 101357 7 15.4 81.1 407 20 709331 8 15.4 81.1 407 20 709331 8 15.4 81.1 461 22 R50055 10 15.4 81.1 267 22 R5466 11 15.4 81.1 267 22 R50456 11 15.4 81.1 267 22 RA00904 11 15.4 81.1 360 30 AA241 15 15.4 81.1 303 31 AA2991 17 15.4 81.1 303 31 AA2991 18 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 485 37 AA6835 19 15.4 81.1 495 41 A10494 20 15.4 81.1 403 42 A11533 21 15.4 81.1 403 42 A11533 22 15.4 81.1 403 42 A11533 23 15 78.9 302 31 AA352 24 16.8 77.9 325 24 N33044 25 16.8 77.9 425 25 AA0465 33 14.8 77.9 425 27 AA0465 33 14.8 77.9 325 32 AA352 34 14.8 77.9 325 32 AA352 35 14.8 77.9 355 32 AA352 36 14.8 77.9 451 33 AA442 14.8 77.9 563 33 AA442 14.8 77.9 563 33 AA442 14.8 77.9 563 33 AA442                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |               | . 6   | 9          | ·ω         | ως       | 39370         |
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| 8 15.4 81.1 408 21 T79293 10 15.4 81.1 267 22 R58466 11 15.4 81.1 267 22 R58466 11 15.4 81.1 267 22 R58466 11 15.4 81.1 267 22 R58466 11 15.4 81.1 268 23 AA0290 13 15.4 81.1 303 31 AA2291 15.4 81.1 303 31 AA2291 15.4 81.1 303 31 AA2291 15.4 81.1 303 31 AA2391 15.4 81.1 428 32 AA3509 17 15.4 81.1 459 41 AI0494 20 15.4 81.1 469 41 AI0494 21 15.4 81.1 469 42 AI1533 22 15.4 81.1 403 42 AI1533 23 15 78.9 280 20 D26711 24 15 78.9 302 31 AA3297 25 17 14.8 77.9 425 24 N33046 29 14.8 77.9 425 24 N33046 29 14.8 77.9 313 26 W25333 31 14.8 77.9 327 AA046 33 14.8 77.9 329 327 AA046 34 14.8 77.9 359 32 AA3291 36 14.8 77.9 359 32 AA3291 37 14.8 77.9 359 32 AA3291 38 14.8 77.9 359 33 AA4324 40 14.8 77.9 451 33 AA4324 41 14.8 77.9 563 39 AA8866                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 7             | 5     | μ,         | 0          | 20       | 9332          |
| 9 15.4 81.1 267 22 R50465 11 15.4 81.1 267 22 R50465 11 15.4 81.1 267 22 R50465 11 15.4 81.1 278 28 AA0904 12 15.4 81.1 560 30 AA2441 14 15.4 81.1 342 30 AA2441 15 15.4 81.1 303 31 AA2591 17 15.4 81.1 379 34 AA655 18 15.4 81.1 459 41 AI0485 20 15.4 81.1 459 41 AI0485 21 15.4 81.1 459 41 AI0485 22 15.4 81.1 459 42 AI1533 23 15 78.9 280 20 D26711 24 15 78.9 302 31 AA3279 25 16 17 78.9 502 847 AI0485 26 17 79 327 24 D65439 27 14.8 77.9 327 24 D65439 28 14.8 77.9 312 31 AA3043 31 14.8 77.9 312 32 AA3523 31 14.8 77.9 312 31 AA3043 31 14.8 77.9 312 31 AA3043 31 14.8 77.9 355 32 AA3523 31 14.8 77.9 355 32 AA3523 31 14.8 77.9 356 35 U92781 44 14.8 77.9 563 33 AA4422 44 14.8 77.9 563 39 AA4421 44 14.8 77.9 563 39 AA4826                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ••            | 5     | ۲          | 0          | 21       | 929           |
| 10. 15.4 81.1 267 22 R58460 11 15.4 81.1 278 28 AA0028 12 15.4 81.1 278 28 AA0028 13 15.4 81.1 379 28 AA0290 14 15.4 81.1 342 30 AA2441 15 15.4 81.1 38 30 AA2611 15 15.4 81.1 428 32 AA3500 18 15.4 81.1 379 34 AA455 19 15.4 81.1 379 34 AA455 20 15.4 81.1 459 47 AA083 21 15.4 81.1 683 42 A1153 22 15.4 81.1 683 42 A1153 23 15.4 81.1 683 42 A1153 24 15 78 9 302 21 AA327 25 15 78 9 302 31 AA327 26 15 78 9 302 31 AA327 27 14.8 77.9 327 24 D65438 28 14.8 77.9 425 22 N3975 30 14.8 77.9 313 26 W25333 31 14.8 77.9 320 27 C01356 32 14.8 77.9 320 27 C01356 33 14.8 77.9 320 27 AA0462 34 14.8 77.9 37.9 38.3 31 AA3288 36 14.8 77.9 453 33 AA4422 47 14.8 77.9 563 33 AA4422 48 14.8 77.9 563 33 AA4422 44 14.8 77.9 563 33 AA4422 44 14.8 77.9 563 33 AA4422                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |               | 5     | ۲          | σ          | 22       | 8             |
| 11 15.4 81.1 278 28 AAO904 13 15.4 81.1 560 30 AA241 14 15.4 81.1 560 30 AA241 15 15.4 81.1 188 30 AA261 15 15.4 81.1 188 31 AA299 17 15.4 81.1 303 31 AA299 18 15.4 81.1 303 31 AA299 18 15.4 81.1 428 37 AA683 19 15.4 81.1 485 47 AA683 20 15.4 81.1 465 41 AI0499 21 15.4 81.1 683 42 AI153 22 15.4 81.1 403 42 AI153 23 15 78 9 280 20 D2671 24 15 78 9 302 31 AA350 25 15 78 9 900 50 AU067 27 14.8 77.9 425 24 N3304 29 14.8 77.9 425 24 N3304 29 14.8 77.9 327 AA046 33 14.8 77.9 329 AA046 33 14.8 77.9 329 AA046 34 14.8 77.9 429 AA046 35 14.8 77.9 353 31 AA350 36 14.8 77.9 355 32 AA352 38 14.8 77.9 451 33 AA442 40 14.8 77.9 563 33 AA442 41 14.8 77.9 563 33 AA442 41 14.8 77.9 563 33 AA442 44 14.8 77.9 563 33 AA442                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 10            | 5     | ۲          | σ          | 22       | 8460          |
| 12 15.4 81.1 560 30 AA2418 14 15.4 81.1 1 342 30 AA2418 15.4 81.1 1 188 30 AA2418 15.4 81.1 1 188 31 AA2918 17 15.4 81.1 1 32 31 AA2918 17 15.4 81.1 428 32 AA350 18 15.4 81.1 428 32 AA350 19 15.4 81.1 459 41 AI0494 20 15.4 81.1 459 41 AI0494 21 15.4 81.1 683 42 AI153 22 15.4 81.1 459 41 AI0494 21 15.7 8.9 280 20 D2671 24 15 78.9 900 50 AU0672 25 15 78.9 900 50 AU0672 26 15 78.9 900 50 AU0672 27 14.8 77.9 327 24 D65433 28 14.8 77.9 327 24 D65433 30 14.8 77.9 313 26 W25453 31 14.8 77.9 312 26 W25453 31 14.8 77.9 312 27 AA0462 32 14.8 77.9 312 31 AA3101 36 14.8 77.9 453 32 AA352 38 14.8 77.9 453 33 AA442 40 14.8 77.9 586 35 U9278 44 14.8 77.9 580 39 C8481                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | <u> </u>      | 5     | ۲          | 4          | 27       | 0029          |
| 13. 15.4 81.1 560 30 AA2441 15.4 81.1 188 30 AA2441 15.4 81.1 188 30 AA2441 15.4 81.1 188 30 AA2441 15.4 81.1 188 30 AA261 15.4 81.1 428 32 AA3502 18 15.4 81.1 429 34 AA6852 19 15.4 81.1 45.9 41 A10432 15.4 81.1 683 42 A11533 15.4 81.1 683 42 A11533 15.4 81.1 683 42 A11533 15.4 81.1 683 42 A11533 15.4 81.1 683 42 A11533 15.7 8.9 302 31 AA3275 16.8 77.9 302 31 AA3275 16.8 77.9 325 A26 A26 A26 A26 A26 A26 A26 A26 A26 A26                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 12            | 5     | Ë          | 7          | 28       | 0904          |
| 14. 15.4 81.1 342 30 AA2644<br>15.4 81.1 188 30 AA2644<br>16. 15.4 81.1 303 31 AA299<br>17. 15.4 81.1 303 31 AA299<br>18. 15.4 81.1 428 37 AA683<br>19. 15.4 81.1 485 47 AA683<br>20. 15.4 81.1 403 42 A1153<br>21. 15.4 81.1 403 42 A1153<br>22. 15.4 81.1 403 42 A1153<br>23. 15. 78.9 302 31 AA372<br>24. 15.7 78.9 302 31 AA394<br>25. 15. 78.9 302 31 AA394<br>27. 14.8 77.9 425 24 N3304<br>29. 14.8 77.9 425 24 N3304<br>29. 14.8 77.9 327 AA046<br>30. 14.8 77.9 327 AA046<br>31. 14.8 77.9 329 AA1499<br>34. 14.8 77.9 429 AA1499<br>35. 14.8 77.9 329 AA352<br>36. 14.8 77.9 329 AA352<br>37. 14.8 77.9 35.3 32 AA352<br>38. 14.8 77.9 45.3 33 AA4422<br>40. 14.8 77.9 56.3 39 AA8866<br>40. 14.8 77.9 56.3 39 AA8866<br>41.8 77.9 56.3 39 AA8866                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | _             | .5    | Ë          | 6          | 30       | 2418          |
| 15. 4 81.1 188 30 AA2619 17 15.4 81.1 303 31 AA29819 17 15.4 81.1 379 34 AA4559 18 15.4 81.1 428 37 AA659 19 15.4 81.1 459 41 AI0494 20 15.4 81.1 459 41 AI0494 21 15.4 81.1 459 41 AI0494 21 15.4 81.1 468 42 AI1533 22 15.4 81.1 403 42 AI1533 23 15 78 9 280 20 D2671 24 15 78 9 900 50 AU0672 25 15 78 9 900 50 AU0672 26 15 78 9 900 50 AU0672 27 14.8 77 9 327 24 D65433 28 14.8 77 9 327 24 D65433 30 14.8 77 9 313 26 W25433 31 14.8 77 9 313 26 W25333 31 14.8 77 9 312 27 C01356 32 14.8 77 9 327 27 AA0462 33 14.8 77 9 327 31 AA3101 36 14.8 77 9 453 33 AA4422 40 14.8 77 9 453 33 AA4422 41 14.8 77 9 586 35 U9278 44 14.8 77 9 580 39 C8481                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | _             | 5     | ۲          | 4          | 30       | 2448          |
| 16 15.4 81.1 303 31 AA3505 18 15.4 81.1 428 32 AA3505 18 15.4 81.1 479 34 AA6838 20 15.4 81.1 485 37 AA6838 20 15.4 81.1 485 34 AA6838 20 15.4 81.1 683 42 AI1533 22 15.4 81.1 683 42 AI1533 22 15.4 81.1 683 42 AI1533 23 15 78.9 302 31 AA3275 24 15 78.9 302 31 AA3275 25 16 78.9 900 50 AU0677 27 14.8 77.9 425 24 N3304 28 14.8 77.9 425 24 N3304 31 14.8 77.9 313 26 W25334 31 14.8 77.9 313 26 W25334 31 14.8 77.9 327 CO1353 32 14.8 77.9 329 AA0462 33 14.8 77.9 320 AU0673 34 14.8 77.9 320 AU0673 35 14.8 77.9 320 AU0673 36 14.8 77.9 320 AU0673 37 14.8 77.9 320 AU0673 38 14.8 77.9 320 AU0673 39 14.8 77.9 320 AU0673 39 14.8 77.9 320 AU0673 31 14.8 77.9 320 AU0673 31 14.8 77.9 320 AU0673 32 14.8 77.9 320 AU0673 33 14.8 77.9 320 AU0673 34 14.8 77.9 320 AU0673 35 14.8 77.9 320 AU0673 36 14.8 77.9 320 AU0673 37 14.8 77.9 320 AU0673 38 14.8 77.9 320 AU0673 39 AU0673 40 14.8 77.9 320 AU0673 41 14.8 77.9 560 39 AU0673 42 14.8 77.9 560 39 AU0673                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ь             | 5     | Ľ          | æ          | 30       | 2614          |
| 18.4 81.1 428 37 AA350 19 15.4 81.1 428 37 AA683 20 15.4 81.1 455 47 AA683 20 15.4 81.1 455 47 AA683 20 15.4 81.1 465 42 AI153 21 15.4 81.1 403 42 AI153 22 15.4 81.1 403 42 AI153 22 15.4 81.1 403 42 AI153 23 15 78 9 302 31 AA327 25 15 78 9 900 50 AU067 27 14.8 77.9 327 24 D6543 28 14.8 77.9 425 24 N3304 29 14.8 77.9 127 26 W25453 31 14.8 77.9 127 26 W25453 31 14.8 77.9 329 27 AA0462 32 14.8 77.9 329 27 AA0462 33 14.8 77.9 320 29 AA1499 35 14.8 77.9 409 31 AA328 36 14.8 77.9 409 31 AA328 37 14.8 77.9 451 33 AA4422 41 14.8 77.9 563 33 AA4422 41 14.8 77.9 563 33 AA4422 41 14.8 77.9 563 33 AA4422 41 14.8 77.9 563 33 AA4422 41 14.8 77.9 563 33 AA4422 44 14.8 77.9 563 33 AA4422                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ш             | 5     | ۲          | 0          | 31       | 2998          |
| 15.4 81.1 379 34 AAA552 19.15.4 81.1 459 41 AI0499 20.15.4 81.1 459 41 AI0499 21.15.4 81.1 683 42 AI1533 22.15.4 81.1 683 42 AI1533 23.15.78.9 320 D26711 24.8 17.9 30.2 31 AA3272 25.15.78.9 90.0 50 AU0672 26.15.78.9 90.0 50 AU0672 27.14.8 77.9 455 25 N99752 28.14.8 77.9 455 25 N99753 28.14.8 77.9 313 26 W25333 31.14.8 77.9 313 27 AA0466 39.14.8 77.9 39.3 27 AA0466 39.14.8 77.9 312 31 AA3204 35.14.8 77.9 312 31 AA3204 36.14.8 77.9 355 32 AA324 37.14.8 77.9 355 32 AA3264 38.14.8 77.9 355 32 AA3264 39.14.8 77.9 451 33 AA4326 40.14.8 77.9 583 33 AA4326 41.8 77.9 583 33 AA4326 42.14.8 77.9 583 33 AA4326 43.14.8 77.9 583 33 AA4326 44.14.8 77.9 583 33 AA4326 44.14.8 77.9 583 33 AA4326 44.14.8 77.9 583 33 AA4326                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 17            | .5    | <u> </u>   | ı          | 32       | 3509          |
| 15.4 81.1 485 37 AANSS 27 14.8 77.9 312 72 AANSS 27 AANSS 28 AANS 28 A | . 18          | າຸຕ   | ت          | <b>~</b>   | ω 4      | 5555          |
| 15.4 81.1 633 42 A11533 22 15.4 81.1 633 42 A11533 22 15.4 81.1 403 42 A11533 22 15.4 81.1 403 42 A11533 22 15.4 81.1 403 42 A11533 23 15 78.9 280 20 D26711 24 15 78.9 302 31 AA327 25 14.8 77.9 425 24 D6543 26 14.8 77.9 455 22 A1304 27 14.8 77.9 313 26 W25334 31 14.8 77.9 313 26 W25334 31 14.8 77.9 393 27 C01353 31 14.8 77.9 393 27 C01353 32 14.8 77.9 393 27 AA3045 33 14.8 77.9 312 31 AA3043 35 14.8 77.9 327 31 AA3043 36 14.8 77.9 400 31 AA328 37 14.8 77.9 453 33 AA4328 40 14.8 77.9 453 33 AA442 41 14.8 77.9 563 33 AA442 42 14.8 77.9 563 33 AA442 43 14.8 77.9 563 33 AA442 44 14.8 77.9 563 33 AA442                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ب د           | n U   | ٠.         | пα         | ٠,       | ວິດ           |
| 22 15.4 81.1 403 42 A1532<br>23 15 78.9 280 20 D2671<br>24 15 78.9 30.2 31 AA3272<br>25 15 78.9 628 47 A14857<br>26 15 78.9 900 50 AU0672<br>27 14.8 77.9 495 24 N3304<br>4.8 77.9 455 25 N99753<br>30 14.8 77.9 127 26 W25455<br>31 14.8 77.9 127 26 W25455<br>32 14.8 77.9 313 26 W25455<br>33 14.8 77.9 393 27 AA0462<br>34 14.8 77.9 393 27 AA0462<br>35 14.8 77.9 312 31 AA304<br>36 14.8 77.9 322 AA1494<br>37 14.8 77.9 400 31 AA328<br>38 14.8 77.9 451 33 AA4422<br>40 14.8 77.9 453 33 AA4422<br>41 14.8 77.9 563 39 AA84864<br>42 14.8 77.9 563 39 AA84864                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |               | JS (  | -:         | æυ         | 4 4      | 2 to 42       |
| 23 15 78.9 280 20 D2671 24 15 78.9 302 31 AA327 25 15 78.9 628 47 AI485 26 15 78.9 900 50 AU067 27 14.8 77.9 327 24 N3304 28 14.8 77.9 455 25 N9975 33 14.8 77.9 313 26 W25333 31 14.8 77.9 323 27 AA046 33 14.8 77.9 393 27 AA046 33 14.8 77.9 393 27 AA046 34 14.8 77.9 32 31 AA304 35 14.8 77.9 32 31 AA304 36 14.8 77.9 37.2 31 AA304 37 14.8 77.9 37.2 31 AA304 38 14.8 77.9 37.2 31 AA304 39 14.8 77.9 35.5 32 AA352 40 14.8 77.9 451 33 AA432 41 14.8 77.9 586 35 U9278 42 14.8 77.9 583 33 AA432 43 14.8 77.9 583 33 AA432 44 14.8 77.9 583 33 AA432 45 14.8 77.9 583 33 AA432 46 14.8 77.9 583 33 AA432 47 14.8 77.9 583 33 AA432 48 14.8 77.9 583 33 AA432 49 14.8 77.9 583 33 AA432 40 14.8 77.9 583 33 AA432 41 14.8 77.9 583 33 AA432                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | N             | S :   | Ρ!         | 0          | 42       | 53            |
| 24 15 78.9 302 31 AA32755 25 15 78.9 900 50 AU06736 26 15 78.9 900 50 AU06736 27 14.8 77.9 327 24 D65439 28 14.8 77.9 495 24 N93046 29 14.8 77.9 495 25 N93046 29 14.8 77.9 313 26 W25334 31 14.8 77.9 313 27 AA0463 32 14.8 77.9 380 27 C01356 34 14.8 77.9 380 27 C01356 34 14.8 77.9 380 27 C01358 35 14.8 77.9 327 31 AA30049 36 14.8 77.9 272 31 AA310149 37 14.8 77.9 372 31 AA310149 38 14.8 77.9 47.9 37.9 37.3 AA35215 39 14.8 77.9 453 33 AA44211 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 35 U92781 43 14.8 77.9 586 35 U92781 44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 2             | -     | 8          | œ          | 20       | 712           |
| 25 15 78.9 628 47 A148502 26 15 78.9 628 47 A148502 27 14.8 77.9 327 24 D65439 28 14.8 77.9 495 24 N33046 29 14.8 77.9 313 26 W25334 31 14.8 77.9 313 26 W25453 32 14.8 77.9 313 26 W25453 33 14.8 77.9 393 27 CA04661 33 14.8 77.9 390 27 CA04661 34 14.8 77.9 390 27 CA0368 34 14.8 77.9 429 29 AA14948 35 14.8 77.9 312 31 AA30038 36 14.8 77.9 372 31 AA310139 37 14.8 77.9 372 31 AA310139 38 14.8 77.9 453 33 AA442613 40 14.8 77.9 453 33 AA442613 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 35 AA88605 44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 24            |       | 8          | 0          | 31       | 2755          |
| 26 15 78.9 900 50 AUG6736 27 14.8 77.9 425 24 N33046 28 14.8 77.9 425 25 N99752 30 14.8 77.9 455 25 N99752 30 14.8 77.9 313 26 W253453 31 14.8 77.9 127 26 W25453 32 14.8 77.9 393 27 AA04621 33 14.8 77.9 393 27 AA04621 34 14.8 77.9 429 29 AA14948 35 14.8 77.9 312 31 AA300438 36 14.8 77.9 312 31 AA321914 37 14.8 77.9 400 31 AA321914 38 14.8 77.9 400 31 AA321914 39 14.8 77.9 453 33 AA442113 40 14.8 77.9 453 33 AA442613 41 14.8 77.9 563 33 AA442613 42 14.8 77.9 563 33 AA482613 43 14.8 77.9 563 33 AA482613 44 14.8 77.9 563 39 AA886050                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 25            |       | 00         | N          | 47       | 8502          |
| 28 14.8 77.9 495 24 N99752 39 14.8 77.9 455 25 N99752 39 14.8 77.9 127 26 W25353 31 14.8 77.9 127 26 W25453 32 14.8 77.9 327 AA04651 33 14.8 77.9 393 27 AA04651 34 14.8 77.9 429 29 AA14948 35 14.8 77.9 429 29 AA14948 36 14.8 77.9 429 29 AA14948 37 14.8 77.9 400 31 AA31019 37 14.8 77.9 400 31 AA32613 39 14.8 77.9 451 33 AA442211 41 14.8 77.9 563 33 AA442613 40 14.8 77.9 563 33 AA442613 41 14.8 77.9 563 39 AA486105 42 14.8 77.9 563 39 AA886105                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | N             | ۰,    |            | 0          | 50       | 6736          |
| 29 14.8 77.9 49.3 24 W3534<br>31 14.8 77.9 31.3 26 W25334<br>31 14.8 77.9 31.3 26 W25334<br>32 14.8 77.9 39.3 27 AAA4621<br>33 14.8 77.9 380 27 C01356<br>34 14.8 77.9 42.9 29 AA14948<br>35 14.8 77.9 42.9 29 AA14948<br>36 14.8 77.9 42.9 29 AA36019<br>37 14.8 77.9 27.2 31 AA31019<br>38 14.8 77.9 47.3 31 AA35215<br>39 14.8 77.9 45.3 32 AA35215<br>39 14.8 77.9 45.3 33 AA44211<br>41 14.8 77.9 586 35 U92781<br>42 14.8 77.9 586 35 U92781<br>43 14.8 77.9 586 39 AA88605<br>44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 7 /           | • •   | ٠.         | ) N        | 2 4      |               |
| 30 14.8 77.9 313 26 W25334 31 14.8 77.9 127 26 W25453 32 14.8 77.9 127 26 W25453 33 14.8 77.9 380 27 C01356 34 14.8 77.9 380 27 C01356 34 14.8 77.9 429 29 AA14948 35 14.8 77.9 429 29 AA14948 36 14.8 77.9 272 31 AA30438 37 14.8 77.9 272 31 AA35215 38 14.8 77.9 453 32 AA35215 39 14.8 77.9 453 33 AA44211 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 35 U92781 43 14.8 77.9 586 35 AA88605 44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 2 6           | ٠.    | ٠:         | πv         | J &      | 7 5           |
| 31 14.8 77.9 127 26 W25453 32 14.8 77.9 380 27 CA04651 33 14.8 77.9 380 27 CO1356 34 14.8 77.9 429 29 AA14948 35 14.8 77.9 312 31 AA30338 36 14.8 77.9 372 31 AA30338 37 14.8 77.9 272 31 AA30289 38 14.8 77.9 400 31 AA32894 39 14.8 77.9 453 32 AA35215 39 14.8 77.9 453 33 AA44261 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 35 U92781 43 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 30            | ٠.    | 7          | <b>–</b> ( | 26       | ω,            |
| 32 14.8 77.9 393 27 AA04621 33 14.8 77.9 390 27 COMMARS 34 14.8 77.9 429 29 AA14948 35 14.8 77.9 312 31 AA30438 36 14.8 77.9 312 31 AA321914 37 14.8 77.9 400 31 AA321914 38 14.8 77.9 355 32 AA35215 39 14.8 77.9 453 33 AA442613 40 14.8 77.9 453 33 AA442613 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 35 U92781 43 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 31            | ٠.    | 7.         | N          | 26       | Ĝ             |
| 33 14.8 77.9 380 27 C01356<br>34 14.8 77.9 429 29 AAA4048<br>35 14.8 77.9 312 31 AA300438<br>36 14.8 77.9 272 31 AA3101.9<br>37 14.8 77.9 400 31 AA3210.9<br>38 14.8 77.9 453 32 AA35215<br>39 14.8 77.9 451 33 AA442613<br>40 14.8 77.9 453 33 AA44271<br>41 14.8 77.9 586 35 U92781<br>42 14.8 77.9 586 35 AAA41080<br>43 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 32            | *     | 7          | ø          | 27       | 4621          |
| 34 14.8 77.9 31.2 31 AA31019 35 14.8 77.9 272 31 AA31019 36 14.8 77.9 272 31 AA32194 37 14.8 77.9 400 31 AA32194 38 14.8 77.9 451 33 AA43663 39 14.8 77.9 451 33 AA44211 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 39 AA88605 43 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ى<br>دى د     | • •   | 1.7        | Jα         | 27       | 356           |
| 36 14.8 77.9 272 31 AA31019 37 14.8 77.9 400 31 AA352894 38 14.8 77.9 451 33 AA43563 39 14.8 77.9 451 33 AA43563 40 14.8 77.9 453 33 AA44211 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 39 AA88605 43 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ω u           | 4.    | ۷.         | → ~        | ب<br>د د | 0438          |
| 37 14.8 77.9 400 31 AA32894 38 14.8 77.9 451 33 AA43563 39 14.8 77.9 451 33 AA44211 40 14.8 77.9 453 33 AA44211 41 14.8 77.9 586 35 U92781 42 14.8 77.9 586 39 AA88605 43 14.8 77.9 560 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 36            | •     | 7          | 71         | 31       | 1019          |
| 38 14.8 77.9 355 32 AA35215<br>39 14.8 77.9 451 33 AA442211<br>40 14.8 77.9 453 33 AA442211<br>41 14.8 77.9 586 35 U92781<br>42 14.8 77.9 586 39 AA74180<br>43 14.8 77.9 563 39 AA88605<br>44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 37            | ٠.    | 7          | 0          | 31       | 2894          |
| 39 14.8 77.9 451 33 AA43663 40 14.8 77.9 453 33 AA44211 41 14.8 77.9 586 35 U92781 42 14.8 77.9 583 38 AA74180 43 14.8 77.9 563 39 AA88605 44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 38            |       | 7.         | ū          | 32       | 5215          |
| 40 14.8 77.9 453 33 AA44211<br>41 14.8 77.9 586 35 U92781<br>42 14.8 77.9 333 38 AA74180<br>43 14.8 77.9 563 39 AA88605<br>44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 39            | *     | 7          | S          | 33       | 3663          |
| 41 14.8 77.9 586 35 U92781<br>42 14.8 77.9 333 38 AAA74180<br>43 14.8 77.9 563 39 AA88605<br>44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 4             |       | 7          | ū          | ü        | 4211          |
| 42 14.8 77.9 333 38 AA74180<br>43 14.8 77.9 563 39 AA88605<br>44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 4             | 4     | 7.         | œ          | 35       | 781           |
| 43 14.8 77.9 563 39 AA88605<br>44 14.8 77.9 580 39 C84819                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 4             |       | 7          | w          | 38       | 4180          |
| 44 14.8 77.9 580 39 C8481                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |               |       | 7          | 6          | 39       | 8605          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 4             | •     | 7          | œ          | 39       | 819           |

#### ALIGNMENTS

| T64274/C  IOCUS  T64274  T64274  T64274  T64274  T64274  T64274  T64274  T64274  TFEB-1995  TFEB-19 |
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| T64274 371 bp mRNA EST yc09b09.rl Stratagene lung (#937210) Homo sap IMAGE:80153 5', mRNA sequence. T64274 g668139 T64274.1 GI:668139                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 17-FEB-1995<br>iens cDNA clone                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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ORIGIN
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           REFERENCE
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JOURNAL
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Best Local (
                                                                                                                                                                                                                                                                                                                                 Matches
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
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g829713
R59018.1 GI:829713
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Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                      human.
                                                                                                                                                  yg96c08.rl Soares inf
IMAGE:41340 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High gality sequence stops: 205 Source: IMAGE Consortium, clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information. Insert Length: 57 Std Error: 0.00
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Location/Qualifiers
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Insert Size: 57
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/db_xref="GDB:483770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Stratagene lung (#937210)"
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94.4%;
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EST.
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 374)

1 (bases 1 to 374)

1 (bases 1 to 374)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chispe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Haltman,M., Kucaba,T., Lacy,M., Le,N., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Size: 1290
High quality sequence stops: 388 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1290 Std Error: 0.00
Seq primer: M13RP1
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Unpublished (1995)
On May 8, 1995 this sequence version replaced
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Scares and M.Fatima Bonaldo." 107 c 95 g 145 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:413881"
/db_xref="taxon:9606"
/clone="IMAGE:41340"
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Schellenberg, K.,
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Pred. No. 66;
0; Mismatches
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  Soares, M.B.,
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Tan,F.,
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 239)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997
                                                                                                                                                                                                                                                             AAJYJ708 239 bp mRNA E:
zt71g10.rl Soares_testis_NHT Homo sapiens
5', mRNA sequence.
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Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
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Insert Size: 1177
High quality sequence stops: 289
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 117
Std Error: 0.00
Seq.primer: M13RP1
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Unpublished (1997)
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88 c 49 g 113 t 1 others
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/clone="IMAGE:236152"
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/db_xref="GDB:3863071"
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Tel: 324
Insert Length: 924
Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 226.
                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 309)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                             H01442 309 bp mRNA
y199h09.s1 Soares placenta Nb2HP
IMAGE:147425 3', mRNA sequence.
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17; Conserv
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                The WashU-Merck EST Project
Unpublished (1995)
On May 9, 1995 this sequence version replaced
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EST.
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56 c 37 g 66 t
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/clone_lib="Soares_testis_NHT"
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/db_xref="GDB:5924753"
/db_xref="taxon:9606"
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94.4%;
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Pred. No. 57;
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Best Local :
                                                                                                                                                 JOURNAL
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zeh0888.seq.F 2
cDNA 5', mRNA s
AI353711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Insert Size: 787
High qality sequence stops: 286
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 787 Std Error: 0.00
Seg primer: Promega -21m13
                                         Department of Laborate
University of Toronto
Banting Institute, 100
Tel: 4169788758
                                                                                                                             Identification and Characterization of Expressed Sequence Tags an Embryonic Zebrafish Heart cDNA Library Unpublished (1999) On Jan 14, 1998 this sequence version replaced gi:1798250.
Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                                                         Ton,
                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                             Fax: 4169785650
                                                                                                    Contact: Liew
                                                                                                                                                                                                                                                                              Danio rerio
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                                                                                                                                                                                                                                                                                                                          AI353711.1
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                                                                                                                                                                                           Liew,C.C.
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/db_xref="GDB:559076"
/db_xref="taxon:9606"
/clone="IMAGE:147425"
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Pred. No. 1
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cDNA Library Danio rerio
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Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local :
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                                                                                                                                                                                                                                                              Contact: Adams, MD
The Institute for Ge
932 Clopper Road, Ga
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g390360
T09332.1
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                      Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nature Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 407)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T09332 407 bp
EST07225 Infant Brain,
5' end, mRNA sequence.
                                                                                                                                                                                                                 Email: mdadams@tigr.org
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                           94004965
                                                                                                                                                                                                                                                                                                                                                                                                   Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C.
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                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="HIBBS49"
/clone=1ib="Infant Brain, Bento a 83 c 98 g 105 t
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135 t
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/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.col1 XL1-Blue mrr'"
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/db_xref="taxon:7955"
                                                                                                                                                                                                   ocation/Qualifiers
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            81.1%;
94.1%;
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Gaithersburg, MD
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Score 15.4; I
Pred. No. 2.1e
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Pred. No. 1.3e+02;
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165 GATGGATGAGCAGAGGG 149
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T79293.1
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                                                              16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 929
High quality sequence stops: 319 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert_Length: 929 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 408)
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                             78
                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                           /sex="male"
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/map="1; 15"
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/db_xref="GDB:469239"
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                                                                            81.18;
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                                                              0;
                                                             Score 15.4; DB 21;
Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                           Length 408;
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AUTHORS
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                                                                                                   322 GATGGATTAACNGAGGGT 339
                                                                                                                      1 gatggattagcagagggt 18
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 R58460 267 bp
G3742 Fetal heart Homo
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R50053.1
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                                                                                                                                                                     16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 461)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 210.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 1389
High quality sequence stops: 210 Source: IMAGE Consortium, LLNL
High quality sequence stops: 210 Source: IMAGE Consortium (info@finage.llnl.gov) for further information.
IMAGE Consortium (info@finage.llnl.gov) for further information.
INSERT Length: 1589
Std Error: 0.00
Seq primer: M13RP1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:153019"
/clone_lib="Soares breast 2NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:565292"
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                                                                                                                                                                                 81.1%;
88.9%;
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                                                                                                                                                                Score 15.4; DB 22;
Pred. No. 2.2e+02;
0; Mismatches 2;
sapiens cDNA clone G3742 5' end, mRNA
                                                                                                                                                                                                   Length 461;
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                 02-MAY-1996
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 446)
1 (bases 1 to 446)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g828518
R58460.1
                                                                                                                                                                                                                                                        AAUU2971 446 bp mRNA EST mg50e04.rl Soares mouse embryo NbME13.5 14.5 clone IVAGE:427230 5', mRNA sequence.
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1 (bases 1 to 267)

1 (wang, D.M., Fung, Y.W., Wang, R.X., Laurenssen, C.M., Ng, S.H., Lam, W.Y., Tsui, K.W., Fung, K.P., Waye, M., Lee, C.Y. and Liew, C.C. Analysis of expressed sequence tags from a fetal human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R58460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: liewcc@utcc.utoronto.ca
Insert Length: 1016 Std Error: 0
Seq primer: GGTGGCGACGACTCCTGGAGGCC
High quality sequence stop: 180.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Laboratory Medicine and Pathobiology University of Toronto Banting Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel: 4169788758
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AA002971.1
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                                                                                                                                                                             house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Note "Vector: Lambda gt22; Site_1: NotI; Site_2: SalI; mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo dT adaptor-primer. SalI adaptors were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333) " 71 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="G3742"
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/lab_host="E. coli Y1090"
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94.1%;
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Pred. No. 1.9e+02;
0; Mismatches 1;
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AA090488
                                      cDNAs from fetal heart (1996)
Unpublished (1996)
On Sep 12, 1996 this sequence
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y0582.seq.F Human
5', mRNA sequence.
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16; Conser
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.linl.gov) for further i
MGI:261782
Contact: Liew CC Department of Laboratory Medicine and Pathobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
Washn-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                               Liew, C.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 314 286 1810
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The WashU-HHMI Mouse EST Project
                                                                                          Eutheria; Primates; 1 (bases 1 to 278)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:427230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                       sequence version
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Pred. No. 2.2e+02;
0; Mismatches 1;
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heart,
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5', mRNA sequence
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1 (bases 1 to 560)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Marrin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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16; Conserv
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Banting Institute, 100 College St.,
Tel: 4169788758
Fax: 4169785650
                                                                                         MGI:420556
Seq primer:
                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
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                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                               Unpublished On May 8, 19
                                                                                                                                                                                                                                                                                                                                              Waterston, R.
The WashU-HHMI Mouse EST Project
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                                               primer: -28ml3 rev2 ET from Amersham h quality sequence stop: 488.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : liewcc@utcc.utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            weeks). cDNA was synthesized using a xhoI-oligo dT adaptor-primer. EcoRI adaptors were ligated, followed digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

37 c 58 g 103 t
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/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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94.1%;
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Pred. No. 2e+02;
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RESULT 14
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mx13a09.rl Soares
5', mRNA sequence.
AA244838
                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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h quality sequence stop: 288.
    Location/Qualifiers
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a 130
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/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                   /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
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AA261440 g1895172
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Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 188)

1 (bases 1 to 188)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thetsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1395029.
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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77 g 76 t
                                                                               constructed and normalized by Bento Soares and M.Fatima
                                                                     and Eco RI sites of the modified pT7T3 vector.
                                                                                                                                                                                    /clone="IMAGE:720411"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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Query Match 81.1%; Score 15.4; DB 30; Length 188;
Best Local Similarity 94.1%; Pred. No. 1.8e+0.2;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 atggattagcagagggt 18
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Db 42 ATGGATGAGCAGAGGGT 26
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Search completed: August 18, 1999, 17:04:46 Job time: 2792 sec

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Title:
Perfect score:
Sequence:
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No.
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                             Query
Score Match Length DB ID
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Copyright (c) 1993 - 1998 Compugen Ltd.
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| 16.4.4<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16.2.2<br>16 | 5.5.5.222                                                                                                                        |
| 33533353333333333333333333333333333333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 100.0<br>87.6<br>82.9<br>81.0<br>81.0<br>81.0<br>80.0<br>80.0<br>80.0<br>80.0                                                    |
| 129440 46127 19259 19373 333834 113889 82010 4127600 90824 70825 704104 70400 204104 4675 22917319 22917319 22917319 23917319 23917319 23917319 23917319 23917319 23917319 24675 7788 11688 11988 11988 11988 11988 11988 11988 11988 11988 11988 11988 11988                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1655<br>1420<br>183057<br>39602<br>130336<br>18633<br>1528<br>1528<br>55721<br>144514<br>211912<br>171236                        |
| 11<br>11<br>11<br>11<br>11<br>11<br>11<br>11<br>11<br>11<br>11<br>11<br>11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 2<br>37<br>34<br>34<br>35<br>42                                                                                                  |
| AC004806 AC00487 AC005547 CITV18420 BYPK1CAP ECOUW93 AE000487 AB023042 SPBC1734 SPBC1734 SPBC1734 SPBC137 ATT16113 ATT26818 HS780M13 HUU95737 AC006595 CNS0000A DDU20608 HS780M03 HUU95737 AC006527 AC006527 AC006527 AC006927 AP00005 HPKATTA SYCSITA AC00597 AF068057 AF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | BBU62900<br>AF080564<br>AF127019<br>HSAC000373<br>AC006346<br>CELT24C12<br>BS16086<br>T1F15<br>HS1018D12<br>AC007437<br>AC007656 |
| Homo cheric Eschel Arabic Arabic Arabic Homo Homo Homo Homo Homo Homo Homo Hom                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | rrelia Anoph Homo Humar Homo Bacill Arabic Homo Homo Homo                                                                        |

### ALIGNMENTS

| JOURNAL                                          | TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | REFERENCE<br>AUTHORS                                                                                                                                                           | VERSION KEYWORDS SOURCE ORGANISM                                                      | AE001168<br>LOCUS<br>DEFINITION<br>ACCESSION                                                                                  |
|--------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| burgdorfer1<br>Nature 390 (6660), 580-586 (1997) | Gwinn,M., Dougherty,B., Tomb,JF., Fleischmann,R.D., Gwinn,M., Dougherty,B., Tomb,JF., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Yugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Arthach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K., Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C. Genomic sequence of a Lyme disease spirochaete, Borrelia | Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia<br>burgdorferi group.<br>1 (bases 1 to 13271)<br>Fraser.C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., | 92688598<br>AE001168.1 GI:2688598<br>Lyme disease spirochete.<br>Borrelia burgdorferi | AE001168 13271 bp DNA BCT 15-DEC-1997<br>Borrelia burgdorferi (section 54 of 70) of the complete genome.<br>AE001168 AE000783 |

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MEDLINE
REFERENCE
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Praser.C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A.,
Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,
Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D.,
Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,
Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D.,
Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L.,
Artiach,P., Bowman,C., Garland,S., Fujil,C., Cotton,M.D., Horst,K.,
Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NENUFYDYQESFQRNFLIDLKIVFKDAGLTLEDEIESHINSLMSFKMEKALKDISELR
NSFFRLLQNFKMTSGRLSRIITDLHESVLKTRMLDISNIFSRFTRVVRDLSKKLNKIV
NLKMEGEEFELDKSVIDDLVDPLMHCVRNSMDIGLETVEERVKRGKSKATIILAKNI
EGNVISIEIEDDGIGIDPKVIRRKLIEKGTIKEDAIYSDFELINLIFAPGFSTAVQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNFDFTEDEISDLLLEVENQKLFKVRLDFVKDNPMATISGLQMLQALKSLGKIFKSIP
DSSELLADKFFDFVIYYLISNTSEESIAKKINLPDVVSHFEIKNVNLESLKSVRLKED
DEAPFKENKNIKKNSFISVNLIRIDSKKIDYILNLVSEAVISKSSYNQINSEMITLFY
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/note="similar to PID:1113815 SP:Q44737 GB:AE000783
percent identity: 99.31; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BB0669"
1168. .3762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BB0668"
66. .1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLSGRGVGLDVVKKSIEKLNGTILVESEIGLGTIFKIKLPLTLVIIQGLLVKSGSETY
VIPLNNVLETHRITEHDIKLLENYHEVYNLRDEVISYLRLDKLFNITRDDSLIEKFLI
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/note="similar to GP:1575447 percent identity:
/notified by sequence similarity; putative"
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/note="similar to GP:1881576 percent identity: 98.93;
identified by sequence similarity; putative"
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3769. . . 5169
                                                                                                                                                                                                                                                                                                                                                                                        DLQKDTKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                         VVNTSNMKIAIVVDSILGEEDFVVKPIKDKFSSSAGIVGATTLGNGKVVLIIDVFKLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11/
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codon_start-1
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5706. .6146
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GNFVTTLHAKGFVFDITPPAFIYGENMKISNKGSEALIVPFSLPDGKIIEVNIAIRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="BB0671"
5181. .5666
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FIKEKSTKYFNLYRKV"
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FNYGEEEKLLKPGQNFVEKSDFVSDCDNLDILBNSKNDFSNKVSSKNDGNNENSTLNN
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                                                                                                                                                                                                                                                        /gene="BB0674"
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/gene="BB0673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIQKTTIAADSSSKPRGINYDTGIPFNVLIVDDSVFTVKQLTQI
FTSEGFNIIDTAADGEEAVIKYKNHYPNIDIVTLDITMPKMDGITCLSNIMEFDKNAR
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identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6187. .6702)
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/protein_id="AAC67021.1"
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/transl_table=11
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                                                                                                                                                                                                 putative"
                                                                                                                                                                                                               /gene="BB0674"
/note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                        ISNEMIFFPRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GP:1408275 percent identity:
identified by sequence similarity; putative"
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                                                                                                                                                                 'codon_start=1
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                             'db_xref="GI:2688610"
                                                                                                                                                                                                                                                                                   .7745)
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                                                                                                                                                                                                                           identified by Glimmer;
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gene CDS gene

gene

Sg

CDS

gene

CDS gene

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SOURCE
ORGANISM
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial cds.
U62900
g1575445
                                                                                                                                                                                                                                                                               burgdorferi group.

1 (bases 1 to 1655)

Ge,Y. and Charon,N.W.
An unexpected flaA homolog is present and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BBU62900 1655 bp DNA BCT 15-JAN-1997
Borrelia burgdorferi flagellar filament outsheath protein (fl
gene, complete cds, and chemotaxis histidine kinase (cheA) ge
                                                                                                                          Submitted (03-JUL-1996) Yigong (Microbiology, HSCN, Morgantown,
                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia
                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                   burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                         Lyme disease spirochete.
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                                                                                                                                                                                                         (bases 1 to 1655)
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7739. .8602)
/gene="BB0675"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:L42023 SP:P44755 PID:1004013 PID:1222502 PID:1204815 percent identity: 25.58; identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7739. .8602)
/gene="BB0675"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFDT1F1FLYK1TKAYLSQRLE1YVRNNLFFD1IHCLIPLAFYSSYQLKN1IVAHE
T1LNP1MLSLFKLRFLRLLFFNDL1IE1YYNSKEKNLIL1AFAKAFFSMSLLIPFTFFI
I1SKSKIVNS1DEKQDFN1IKNISIINEKAYLFEKYPFILLIKEKDD1IYYSKSDETFY
YYSPSEYRV1EMEKTKFYIDKYLQRKSDS1LG1FLFTLFASFT1FLMNFYKFFKASFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8599. .9261)
/gene="BB0676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELSEIAKVNKW"
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FNFVKVNSSLRKEFFYNFNTISNGYITFYINKLFEGKNSYTIYLIQKENKALYSSDII
KNYIKILLLLKVLVIKYCFEKGIELTTKNIESTSKAISNDTDFLDEKTAKLIIESFFK
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                                             /strain="212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(8599. .9261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YETLQTMSPISTLIAIFSARARTPKYKNNPVKGFIGYDESWFSIKQSGSREYDSRIIK
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      /clone="pW1 and
                          /db_xref="taxon:139"
                                                                /organism="Borrelia burgdorferi"
                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MNTKPYFPYLYHYLFNHESIKSLSAIEKEIEILNYLKENKKTIA"
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                                                                                       . 1655
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Pred. No.
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                                                                                                                          , Ge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted coding region BB0675"
                                                                                                                          West Virginia University, 26506, USA
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AF080564/c
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AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                               N Anopheles gambiae S. complete cds. AF080564 g3420833
                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGATAAATAATTGGAGCGT 729
1 (bases 1 to 1420)
Devenport, M.P. and Eggleston, P.
Direct Submission
Submitted (29-JUL-1998) School of Biological Sciences, University
of Liverpool, Donnan Laboratories, Liverpool L69 7ZD, UK
                                                                                                 Anopheles gamblae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Culicidae; Anopheles.
                                                                                                                                                                                African malaria mosquito.
                                                                                                                                                                                                                         AF080564.1
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/gene="cheA"
1566. .>1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="flaa protein"
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DNIKTMKEIKYSVYSLGYEIDLEVLFEDMNGKEYAYSMGTLKFGWADLIWSNENYID
DNIKTMKEIKYSVYSLGYEIDLEVLFEDMNGKEYAYSMGTLKFGWADLIWSNENYID
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473. .1498
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SNEGFSFGFLLSDSRFLYSFLKNGVYYVNLSREFYDSFNNGDYNESFDVKVNLFAMSL
IKTMRFNYPGKIKKIIILVEGCILKEQS"
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/protein_id="AAC44769.1"
/db_xref="PID:g1575446"
/db_xref="GI:1575446"
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182 c 308 g 605 t
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/protein_id="AAC44771.1"
/db_xref="PID:g1575448"
/db_xref="GI:1575448"
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/transl_table=11
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                                                                     Submitted (09-FEB-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 1-1298: contig of 1298 bg; 1289-1299: gap of unknown size 1299-36867: contig of 35569 bp; 36867-36868: gap of unknown size 16868-124154: contig of 87287 bp; 124154-124155: gap of unknown size 1299-36867-124155-149039: contig of 24885 bp; 149039-149040: gap of unknown size 149040-151546: contig of 2507 bp; 151546-151547: gap of unknown size 149040-151546: contig of 1507 bp; 151546-151547: gap of unknown size 151547-183057: contig of 31511 bp;

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence to severe the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the se
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1 (bases 1 to 183057)

Taudien,S., Nordsiek,G., Schlegelberger,B., Drescher,B., Weber,J., Schattevoy,R., Menzel,U. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARILA/ULY 183057 bp DNA
HTG 28-FEB-1999
Homo sapiens chromosome 8 clone PAC 188E4 map 8p23, WORKING DRAFT
SEQUENCE, in unordered pieces.
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Location/Qualifiers
1. .183057
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/protein_id="AAC31944.1"
/db_xref="GI:3420834"
/db_xref="GI:3420834"
/db_xref="GI:3420834"
/db_xref="GI:3420834"
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YFPESTYAPMIYPGTPHQAHYSPQSYRPLAGAGATSYNNSTSTSPQDLSTASGG
YCAPANDGNNGRPEISPKLSPGSVESVGSSGNSTANNSTTSPQDLSTASGG
SGRANDGNNGRPEISPKLSPGSVSVGSGGSSSKKGGFPPHIYPMKRVHIGQSTVNA
NGETKRQRTSYTRYQTLELEKEFHFNNYLTRNRRIEIAHALCLTERQIKIMFQNRRMK
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262. .1380
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95.0%;
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental complement(7339. 7554) /rpt_family="MIR" /evidence=not_experimental complement(7645...7895)
                                                                                                                               /evidence=not_experimental complement(9988..10323) /rpt_family="MLT1A2"
                                                                                                                                                                                                             /evidence=not_experimental
complement(8309..8587)
/rpt_family="L1PB1"
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6744. .6835
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complement(1614 . 1678)
/note="GRAIL, score = 57.0
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/evidence=not_experimental
complement(1178. 1343)
/rpt_family="MER5A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Xpound exon prediction,
/evidence=not_experimental
complement(5495...6325)
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/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental 2761. .3051
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complement(10340.
                        /note="Xpound exon prediction, score = 69% (0%)"
/evidence=not_experimental
                                                                             /evidence=not_experimental
complement(10104. .10169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6226. .6306
/note="MZEF, score = 94%"
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/note="GRAIL,
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/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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/note="MZEF, score = 92.3%"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="PAC 188E4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="Alux"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="MIR"
                                                                                                                                                                                                                                                                          _family="Alux"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score = 59.000%,
.10443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comment -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comment = good"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score = 77% (0%)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comment = Terminal_exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               good shadow"
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exon

repeat\_region

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/note="GRAIL, score = 99.000%, c
/evidence=not_experimental
complement(22868. 22962)
/note="GRAIL, score = 89.000%, c
/evidence=not_experimental
complement(23081. 23195)
/rpt_family="L2"
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/evidence=not_experimental
/evidence=not_experimental
complement(13288. .13412)
/rpt_family="fl2"
/rpt_family="fl2"
                                                                                                                                                                                                                                                                                                             /note="MZEF, score = 50.5%"
/evidence=not_experimental
complement(21617. .21918)
/rpt_family="Aluy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence-not_experimental complement(18568. .18634) /note-"xpound exon prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
complement(18091..18172)
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/rpt_family="L2"
                                                                                                                                                                                                                                                                       /evidence-not_experimental complement(21820. .21979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp frame: 2 phase: 1"
/evidence=not_experimental
complement(18091. .18172)
/note="MZEF, score = 77.2%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MZEF, score = 90.7%"
/evidence=not_experimental
17635 .17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
12987. .13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="GRAIL, score = 47.000%, comment = marginal shadow"
/evidence=not_experimental
10459...10563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
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                                                                                                                                                                    /evidence=not_experimental
                                                                                                                                                                                          /note="MZEF, score = 54.4%"
                                                                                                                                                                                                             /evidence=not_experimental
22117. .22184
                                                                                                                                                                                                                                                      note="MZEF, score = 66.8%"
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18444. .18515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="GenScan, score = 1.48%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MZEF, score = 93.8%"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score = 86% (0%)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comment - Internal_exon 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comment -
                                                                comment - excellent'
                                                                                                                            comment - excellent shadow"
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                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                 COMMENT
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DEFINITION
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HSAC000373/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                      Submitted (12-MAR-1997) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
This entry has been annotated with sequence quality estimates computed by the Phirap assembly program. These values are not generally visible from the Genbank flat file format but are available as part of the ASN.1 file.

Verification: This sequence has been verified by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining descrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                            Large-scale MCD Mapping and Sequencing of Human Chromosome 7 Unpublished (1996)
2 (bases 1 to 39602)
Magness,C.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 39602) Indonato, S.P., Yu, J., W. Green, P. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSAC000373 39602 bp ms-DNA
Human cosmid g1862d218, complete sequence.
                                                              dashed lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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/evidence=not_experimental
28023..28051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence-not_experimental complement(25837. 25870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(24685. .24855)
/rpt_family="MIR"
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bp frame: 1 phase: 1"
/evidence=not_experiment
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/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Xpound exon prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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94.7%;
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wong, G.K.-S., Magness, C.L., Green, E.D.,
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                                                                                                                /rpt_family="MER46"
complement(39085. .39163)
/rpt_family-"MER46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="NCHGR:yWSS1862"
/sub_clone="UWGC:91862d218"
/cell_line="GM10791"
/clone_lib="E. Green Chromosome
5266. 5336
                                                                                               /rpt_family="MER46" 7537 c 760c
                                                                                                                                                                                                                                                                                                                                        /rpt_family="THE1"
complement(20791.
/rpt_family="ALU"
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/rpt_family="ALU"
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5357. 5635
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                                                                                                                                                                                                                                                             23607
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complement(22879.
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7554. .8063
                                                                                                                                                                                                                                                                                                                                                                         /note="Genbank Accession: G13152"
16084. .16489
                                                                                                                                                                                                                                                                                                                                                                                              /standard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                           /rpt_family="L1"
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                                81.0%; Score 17; DB 10;
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                _family="ALU"
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                                                                                                                                                                                                                                                                                                                                                                                               _name="HUMSWS3394"
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||||||||||||||||||
14 TGGGATAAATAATTGGA 86298
             Caenorhabditis elegans strain-Bristol N2.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida; Rhabditida;
Rhabditina; Rhabditoidea; Nematoda; Secernentea; Caenorhabditis.
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1863)
Nibon,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
                                                                                                                                                                                                                                                       g1086755
U41037.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on Jan 28, 1999 this sequence version replaced gi:4139377.

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
U41037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (11-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 130336)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 130336)
Waterston, R.H.
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Latreille, P., Lightning, J.,
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1. .130336
                                                                                                                                                                                                                                                         GI:1086755
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="DJ0820G22"
25513 c 23549 g
                                                                                                                                                                                                                                                                                                                                          18633 bp
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; Pred. No. 1.1e+02;
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Lloyd, C.,
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    Mortimore, B
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The sequence of C. elegan
Unpublished (1995)
3 (bases 1 to 18633)
Waterston, R.
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2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elegans
Nature 368 (6466), 32-38 (1994)
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Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
NEIGHBORING COSMID INFORMATION:
cosmid is F48B9, 200 bp overlap; 3' cosmid is T14F9. Actu
of this cosmid is at base position 26876 of CELF48B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/protein_id="AAA82387.1"
/db_xref="piD:g1086756"
/db_xref="piD:g1086756"
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RSKEWLEMPGAEGMLSLKLTLAQDLLKCINSVEHGQVRVDVDENWKSGPAKWFYLRSK
ANEDGEGGEDGGDIGDATVKVTYQIDHILRMQVKFLLLAGDVQPLTASLVAVI
EALPKVELGFVSRSLVELMAGSBRIRVFLSSLXVNSILKCQDENTLFRGQSLSKMLF
EILTTYGKMYLITTLKPVVDKIYKERKNCEVDPARVAVGASLEKNRNLLLVYFQMLFE
EILTTYGKMYLITTLKPVVDKIYKERKNCEVDPARVAVGASLEKNRNNLLVYFQMLFE
RNTTSSTNCHLIKQLLYDLRNVVGTHSSRSGYQRLAVSSFYIMRFFAAAILNFKAFE
IRKDQPDLRVSRTLLLLSKLLQRLSNCSVSEGFDLSSKEIMLNGVEETVTSSQHKSWA
GFT.NLTGTVGTHSEEDDVFTTVFGNT CONTDEED AUEKUTURVENDYGT AWEKUTURVKTONG
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ed (20-NOV-1995)
/note-"coded for by C. elegans cDNA yk4la1.3; coded for by C. elegans cDNA yk128e3.3; coded for by C. elegans cDNA yk37c8.3; coded for by C. elegans cDNA CEESGA5F; coded for by C. elegans cDNA CEESGA5F; coded for by C. elegans cDNA yk37c8.5; coded for by C. elegans cDNA yk37c8.5; coded for by C. elegans cDNA yk128e3.5; coded for by C. elegans cDNA
                                                                                                                                                                                 /gene="T24C12.3"

complement()oin(10021...10249,10474...10732,10788...10902,

11124...11205,12330...12409,15353...15409,15576...15700,

15747...15832,15916...16036,16089...16322,16453...16564,

16609...16707,16982...17057,17102...17256))

/gene="T24C12.3"
                                                                                                                                                                                                                                                                                                                                             complement(10021. .17256)
/qene="T24C12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                      SFILDNISLVGDRSEPOKCTVFKFGNLQQVDRSRLAWKKVLHYKKRYVQLTNTHLIWOK
DVQCAPKGTVVLSDIK VNVDNKNIITIVCETWOLDGFBAPGGVEATDWLMAIERORNR
AAHELAET9CHFFVDAERHVDKIHTLLYKYRETMIEWRDQLQSUVELDEKTAPELK
ASYVVEEERQSHKDSLIATLCSTIDVTDAIQLAHTEYEKENKVSRRIDAIITAKKRQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="T24C12.2"
Join(5921. .6016.6086. .6399.6938. .7129,7183. .7297,
7349. .7544,7595. .7794,7842. .7970,8020. .8270,8322.
                                                                                                                                                                                                                                                                                                                                                                                                 SFSVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T24C12.2"
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/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
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Bacillus silvestris
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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EEVVHLLKTSKSIGLEYGTILACPIPEKYAADGDA IQAQVQEA IQANASQSVT
PFILARVNEITGASMATUTALLENNASIAGELAGKLCDRRPLTISQSQPTASTTRK
KVVSIGATIVDFEAITSEDVKDDGGSYNGQVVQRMGGVARNHADALARLGCDSVFISA
IGDDNNGHFFRONSHKIVESNEDALESSDFILLDSNLSVPVMARVLEIAKKHDKQVWL
EPTDIDKVKKVEDTGLYGAVTAASPNANEFLKMAKLCHVSVMPSVIDTADGVLELIEK
EXTKLLLNTSIFIVTLANKGSAVVRNKLGQLEFQSLPPPLQNNKVVSVSGAGDSFNS
GETGGLAHNKTYVESLQIGQECARLTLQTSLAISDAITPNLLA"
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complement()oin(17658. .17810,17859. .18036,18102. .18282,

1836. .18480))

/gene="T24C12.4"

/codon_start=1
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KKQTCAFKVFSCSSFFSKIFFRSCFFRAFGKAAMLYGSMNILLAVFLFLGATIVMLT
SPLETVLIPIKKNDFYLGYGE INICLALLCIASIVAIKRQIGVVVFCHMIKCCTLIV
DAVMYFVFASIMSTAHTSLYSHIQVLHNSSKELGSVMDNVQTLICCPPEEVLQTCAD
FLNVTKSFCPFGHSNDCYIHLKRWLHSNTEIVGCLAFCVITPLKLFMIAALFKDIEKV
ETEMABELEYYSGMINEYDHRÜDGY IESFKSNINLADSTSTQTSGISKVKSFPGYSPFL
KHSVIEEVENEFTYRGDEIREELQQAIAAHNAROLEAAAVTEQF"
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/transl=+4~~-""
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/gene="T24C12.4"
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PYPHNLRYTARSLEQKVRSSGSHPATIALFDGKIHVGLDDEKLELLASSQNAVKVSSR
DIAKTLIKKEVGGTTVASTMKIAHAAGISVFATGGIGGVHRGADQTFDVSADLQELSQ
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IFLIHIVDAGFQISQLKPLYKEDNITISELSTALGAAFPPCCSDIISSIACRRLQQHN
PSKFLDRCATDADFSLIQCCNTCGMESAADRYELIFQAGHKSNQCFDRHGSEFCKRFL
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/protein_id="AAA82389.1"
/db_xref="PID:g1086758"
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13855. .13936,13984. .14053,14107. .14262,14312. .14570)
/gene="n24612.1"
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in NFO-FRUA intergenic region (SP:YEIN_ECOLI,P33025)
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||||||||||||||||| | |
TGGGATAAATAATTGGGGTG 1485
                                                                                                                                   This sequence is of BAC TIF15 from Arabidopsis thaliana chromosome 1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 11342 bp because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide a small overlap (200 bp) between overlapping submitted clones. The 3' end of this sequence overlaps by 200 bp the 5' end of the sequence of the BAC FIN21.
                                                                                                                                                                                                                                                                                                                                                                               Vysotskaia, V.S., Schwartz, J.R., Toriumi, M., Yu, G., Oji, O., Kwan, A., Liu, S., Li, J., Araujo, R., Au, M., Berendel, V., Buehler, Conway, A.B., Conway, A.B., Conway, A.B., Conway, A.B., Conway, A.B., Conway, A.B., Coway, A
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Mascheroder Weg 1b, 38124 Braunschweig, FRG
Revised by author 16-NOV-98
Location/Qualifiers
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Submitted (11-MAR-1998) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
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Pred. No. 2.1e+02;
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. 49 Pt 2, 795-802 (1999)
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BAC TIF15 sequence, complete
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Submitted (02-MAY-1998) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Street, Albany, CA 94
4 (bases 1 to 55721)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Translation="MCSNGIFVSLLTLSLLLGKSCSETDTLHOGOFLKDGOELVSAFK
| TEKLKEFNEKKSENLYLGIFENNLYLMTDSQDRPVWIANNNEISDRSGSLTVDSLGR
LKILKGSTMLELSSIETTRNTTLQLLDSGNLQLQEMDAGSMKRVLMQSFDYPTDTL
LPGMKLGFDGKURKRKELTSWLGDTLDASGSFVFGMDTNITNVLTILMGGNMYWSSGL
WNKGRFSEELLNECGFLFSFVSTKSQQYFMYSGDQDDARTFFPTIMIDEQGILRREQM
HRQRNKONYNRRCLAAGYVVRDEPYGFTSFRVTVSSSASNGFVLSGTFSSVDCSAIC
LQNSSCLAYASTEPDGTGCEIWNTYPTNKGSASHSPRTILIRGNGQENKKVAAWHIVV
ATLFLMTPITWFITLKFNYKGRNCIRTHKTVLVSMYFLLTSSPSFFLEMIQDV
FYFVEYTTFYGESSLLKVHQEMLLRELGIDRSCIHKRNEKSNNELQIFSFESVVSAT
DDFSDENKLEBGGFGFYKGKLLNGEEVAIKBLSASGGGLVEKSNEALLIAKLQHTN
DDFSDENKLEBGGFGFYYKGKLLNGEEVAIKBLSASGGGLVEKSNEALLIAKLQHTN
                                                                                                                                   KLCGFPLQKTCKDTDENSPGTRKSPENNADSRRGLSTGLIVLISVADAÄSVAFIGLVL
VYLYWKKDSEGCSCTGNAKLGGGSVKGKSCCCTTGFPKEDSEAECNERGEGKDG
ELVALDKGFSFELDELLFASAAVLGKSGLGIVYKVVLGNGVPVAVRRLGEGEDKYKE
FVTEVQAMGKVKHPNVVKLRAYYWAPDEKLLISDFVNNGSLADALRGRNGQPSPSLTW
STRIKLAKGAARGLAYLHECSPRKLVHGDVKBSNILLDSSFT9YISDFGLTRLITITA
ASASSNEPSSSSAAGGFLGGALPYTSIKPSDNSNGYKAPEARLPGGRPTOKNDVYSFG
VYLMELLTGKSPDSSPLSSSTSTVVVEVPDLVKMVRKGFEEETPLSDMVDPMLLQEV
                                                                                                                                                                                                                                                                                                                                                                               /translation="MILLSLLLHLLLHLLNTSPSLSLSPDGIALLSLKSAVDHSSSSA FSDWNNDTDPCHWSGISCMNISDSSTSRVVGISLAGKHLRGY IPSELGSLIYLRRLN LHNNELYGSIPTQLFWATSLHSIFLYGNNLSGTLPPSICKLFKLQNLDLSMNSLSGTL SPDLNNCKQLGRLILSANNFSGEIPGDIWPELTNLAQLDLSANEFSGEIPKDIGELKS LSGTLNLSFNHLSGQIPNSLGNLPVTVSLDLRNNDFSGEIPQSGSFSNQGPTAFLNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYFREGLFSAKSDVFSFGVLMLEIICGRKNNSFHHDLEGPLNLIVHVWNLFKENKIRE
VIDLSLRDSALDYPQVLRCVQVALLCVQENAEDRPSMLDVVSMIYGEGNNALSLPKEP
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3708...3945,4015...4168,4259...4576)
/gene="TIF15.1"
                                                                                                     HAKQQVLSVFHLALACTEGDPEVRPRMKNVSENIDKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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/db_xref="PID:g3176660"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="T1F15.2"
Join(7204. 8692,9241. .9911)
/gene="T1F15.2"
/note="Similar to_ERECTA receptor protein kinase gb|U47029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFYDGPRRSFPEMKVEPQEPENVSASITITVLEAR"
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HKYSRLKVIHRDIKASNILLDEDMNPKISDFGLARIFGAEETRANTKRVAGTFGYMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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/db_xref="PID:g3176659"
/db_xref="GI:3176659"
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/gene="T1F15.1"
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1. .55721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/chromosome="1"
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   .10785,10946.
.11028,11116.
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   .11173,11269. .11318
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PODGK SPADDU GUMSDY GEGMALKELINKVELSPECKE PECKET AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FALLE AND FAL
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WREHNGRDYGRQELVENDMYLETSFVKSKGDGLGYGGDWAVRIDVKNKGTFVAVSAGS
GSAGGLIFSVMFRMSSAHALDITILIVHLQNOLETHYSGRKPFIGIGTSESSNVE
KRLTSLTGLPLSDLLKKKHQEFDAKFNECFKLSEKHDSETLGVGRTAIANMLGGIGYF
YGQSKIYVFKSTQPGSEDNFLLYWPAELYTAVPSRFFFRGFLMDEGFHQLLTHRWDI
YGQSKIYVFKSTQPGSEDNFLLXWPAELYTAVPSRFFFRGFLMDEGFHQLLTHRWDI
IDAIRMEKFVASEKDEVLSFLEEASVRLDAWFQWFNTSQKGKELGSYFWHGGDNTTTQ
ELLPKTLSSGLDDYPRASHPSEDERHVDLRCMYKLAADCMHSTTELLGKEDKLSKVST
ELLPKTLSSGLDDYPRASHPSEDERHVDLRCMYKLAADCMHSTTELLGKEDKLSKVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(20807. .21106,21194. .21267,21348. .21599,21949. .22
22261. .22350,22448. .22544,22957. .23039,23403. .25510,
23630. .23751,23991. .24008,24085. .24158.24510. .24635,
24886. .24953,25260. .25435,25567. .25711,25831. .25980,
26086. .26177,26254. .26363,26473. .26536,26611. .26755)
//gene="Tiff15.4"
/note="Similar to mannosyl-oligosaccharide glucosidase
gblx87237 from Homo sapiens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYFYLSKHCILCGEVVQESAQLCNRCLQNKSAAAATIVWKTSKLEREMQHLATICRHC
GGGDWVVQSGVKCNSLACSVFYERRKVQKELRGLSSIATESELYPKCMAEWF"
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GQRIDEVAITKANSSAAASVSFPVWSLSTIPGQWMWNLSEESDIPLSQSQHRHQHHYR
RQSLCELEGDATSSDILNQQFKMYNSLSQAQSDTNMVQSLVAIWEEEYERTGVHDAPI
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KGNAASKRQHIHDCEIVRAKKFYGYHSTEEAFVKIYLYPYSSYHPPDVARAASLLLAG
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12547. 12730,12809. 112900,12979.
15191. 15243,15849. 15991,16076.
17063. 17335,17501. 17608,17692.
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join(20807.
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S. cerevisiae."
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.14599,14801..14992,
.16658,16735..16881,
.17897,18107..18410,
                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ğ
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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                                                                                                                                             FEATURES
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HS1018D12/c
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JOURNAL
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                                                                                                                                                                              AL Submitted (02-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk On Jun 3, 1999 this sequence version replaced gi:4837662.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJI018D12 Contig_ID: 01259 acc=AL031650 Length: 142349 bp Unfinished: dJ1018D12 Contig_ID: 03240 acc=AL031650 Length: 1365 bp.

* NOTE: This is a "vorking draft' sequence.

* This record will be updated with the finished sequence will
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1 (bases 1 to 144514)
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ATFYLSVQKIGLKMQAFALSGKKRIVNHGMCFSKGNLDLGSRLSENFMDDPLIPGLPD
DVAKQCLALVPRARFPSMGSVCKKWRFVVQSKEFITVRRLAGMLEEWLYVLTMNAGGK
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/gene="IIF15.5"
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SNRSILWSDYGLVSLAKTSSMYMKRNTEHDAPYWRGPIWMMMYMILSSLYHYSIVDG
PYREKSKAIYTELRSNLIRNVVRNYYETGYIWEQYDQVKGTGKGTRLFTGWSALTLLI
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                        /clone="1018D1
                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                        Location/Qualifiers
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/protein_id="AAC18788.1"
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20 clone 1018D12, WORKING DRAFT SEQUENCE,
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ORGANISM
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AC007437/c
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Direct Submission

Submitted (30-APR-1999) Molecular and Human Genetics, Baylo College of Medicine, One Baylor Plaza, Houston, TX 77030, U On Jun 17, 1999 this sequence version replaced 91:5080739.

* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Homo sapiens, WORKING DRAFT SEQUENCE, 31 unordered pieces.
AC007437
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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83123: gap of u
163418: contig
163438: gap of u
187893: contig
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189387: contig of
189407: gap of u
190763: contig
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Homo sapiens 12q22 BAC RPCII1-534P6 (Rowswell Park Cancer
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-MAY-1999) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicin Baylor Plaza, Houston, TX 77030, USA On May 29, 1999 this sequence version replaced gi:4895152. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OWALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
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9175. .9508
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9103. .9174
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/rpt_family="MIR"
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23574. .23768
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                                                                                                                                                                                                                                                                                                                                                                      L_family="MER5A"
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                                                                                                                                                            .20793)
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Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens 12q24.2 BAC RPCI11-360E11 (ROSWell Park Cancer
                                                                  Direct Submission
                                                                                                Worley, K.C.
                                                                                                                                                             Unpublished
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complement(30657. .30779)
/rpt_family="MLT1A1"
32217. .32245
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/rpt_family="L2"
30273. .30365
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complement(29215. .29371)
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/rpt_family="L2"
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/rpt_family="L2"
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Pred. No. 1.3e+02;
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Worley, K.C.
Direct Submission
Direct Submission
Submitted (20-JAN-1999) Human Genome Sequencing Center, Deposition
Submitted (20-JAN-1999) Human Genetics, Baylor College of Medicine
Medical and Human Genetics, Baylor College of Medicine
Baylor Plaza, Houston, TX 77030, USA
On Oct 30, 1998 this sequence version replaced gi:3327896.
INFORMATION: http://gc.bcm.tmc.edu:8088/home.html or email
                                                                                                                                                                                                       of Molecular and Human
Baylor Plaza, Houston,
4 (bases 1 to 129440)
                                                                                                                                                                                                                                   Submitted (30-OCT-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 129440)
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of Medicine,
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COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. gc-help@bcm.tmc.edu

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and CDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

# QUALSTAT-REPORT----

| Quality                           | Position<br>9274<br>15955<br>51005<br>51240<br>168300                                                                                  | Contig length: Phrap values 1 Average error Fraction of Ph Number of cons Number of N's                                                                                                                            |
|-----------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Position Surrounding S            | Original+Context tottccctt(n)cccttctcct ctttttttt(n)tcctctqaag aaaagtttga(n)ataattttgg acggtgaaac(n)ctgtctctac gctcctctct(n)accccccaga | Contig length: Phrap values in estimate: Phrap values in estimate: Average error rate (BCM.Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus: |
| Quality BasesSurrounding Sequence | Edited+Context tottcccctt(c)cccttctcct ttttttttt(t)tcctctgaag aaaagtttga(a)ataattttga acggtgaaac(c)ctgtctctac gctcctctt(c)accccccaga   | 172045<br>172045<br>83363<br>2.05999e-06<br>0.00133153<br>5                                                                                                                                                        |

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/rpt_family="(TGGA)n"
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complement(14782..14900)
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complement(5117. .5446)
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/rpt_family="L2"
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/rpt_family="L2"
   10303..15402
/note="ct rich region"
/notetion="Gap in sequence of less than 50 bases
containing T(i)C(j) repeats."
15403..15672
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14874.
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/chromosome="12q24.2"
                                                                                                                                                       /function="Low coverage"
                                                                                                                                                                                                                                                                                                                                                              /rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                function="Low coverage"
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/db_xref="taxon:9606"
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AC005547/c
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1 (bases 1 to 46127)

Lamerdin, J. E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,
Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,
Liu, S., Attix, C., Andreise, T., Trankheim, M., Amoroe-Keller, G.,
Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,
Kronmiller, B., Arellano, A., Ow, D., Nolan, M., Trong, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
17; Conserva
                                                                                                                                                                                                                                   Kronmiller, B., Arellano, A., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of an -600 kb human contig in 19q12 between p199430 and D198776
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AC005547.1 GI:3478634
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complement(16381..16500)
/rpt_family="L2"
complement(16501..1676)
/rpt_family="TIGGER2"
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24376..2
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complement(20383. .20678\
/rpt_family=""."
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22099. .22383
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/rpt_family="MERIA"
complement(16947. .17260)
/rpt_family="AluJb"
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complement(22667...
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complement/100.5
/organism="Homo sapiens"
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chromosome
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94.4%;
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                                                      /note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 90.000" complement(16731. .16809)
/rpt_family="MIR"
17248. .17354
  /note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 79.000"
complement(18564. .18597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(11361..11595)
/rpt_family="MER7A"
complement(11596..11950)
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/rpt_family="MLT2FB"
complement(10851..10958)
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/note="predicted exon, |
frame: 0, quality: exce
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                                                                                                                                                                                                                                                                          /rpt_family="AluJo"
complement(14886. ...
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/rpt_family="AluJo"
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/cell_line="5HL2-B"
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/clone="R29228"
/chromosome="19"
                                                                                                                                                                                                                 /rpt_family-"MER81"
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1293. .1444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="LL19NC03 R chromosome 19-specific cosmid
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. .6224
                                                                                                                                                           -_family="THE1C"
7. .16656
                                                                                                                                                                                                                                     ____family="AluSx"
7. .15206
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2. .11320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="MLT2FB"
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                                                                                                                                                                                                                                                                                                                                    _family="(GAAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       .3990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      edicted exon, program: grail2exons_human_1.3,
quality: excellent, score: 78.000"
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d, score: 51.000"
                                        misc_feature
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complement(20628...20673)
/rpt_family="(cAT)n"
complement(20755...20860)
/rpt_family="MIR"
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complement(18599. .19
/rpt_family="L1PA15"
19487. .19728
                                                                                                                                                                                                                                                                                                              34300. .34450
34300. .34450
/note="DDS similarity to overlapping ESTs:-AA824408
/note="DDS similarity to overlapping ESTs:-AA824408
a175e07.s1 Soares testis NHT Homo sapiens cDNA clone
1376676 3'; (153. .1); 99% identity.--AA971001 op67h02.s1
Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1581939
3'; (154. .4); 100% identity."
                                                                                                complement(37245...37307)
/rpt_family="AT_rich"
38183...38246
                                                                                                                                                     /note="predicted exon, pr
frame: 2, quality: good,
complement(37184. 37244)
/rpt_family="(GA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"predicted exon, program: frame: 2, quality: good, score: complement(34259. .34296)
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clone 1376676 3', (463 .154); 99%
identity.--(32501 .32670) AA971001 op67h02.sl
Soares_NFL_T_GBC _S1 Homo sapiens cDNA clone IMAGE:1581939
3', (324. .155); 100% identity."
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                                                                                                                                                                                               program:
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71.000"
                                                                                                                                                                                               grail2exons_human_1.3
73.000"
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56.000"
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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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CITV18420/c
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                 5'UTR
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Vives, M.C., Rubio, L., Lopez, C., Navas-Castillo, J.,
Albiach-Marti, M.R., Dawson, W.O., Guerri, J., Flores, R. and Moreno, P.
The complete genome sequence of the major component of a mild
citrus tristeza virus isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y18420.1 GI:4239714
complete genome; ORF1; ORF10; ORF11; ORF2; ORF3; ORF4; ORF5; ORF6;
ORF7; ORF8; ORF9; pl3 protein; pl8 protein; p20 protein; p23
protein; p25 protein; p27 protein; p33 protein; p349 protein; p65 protein; p65 protein; RdRp protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITV18420
Citrus tri
                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-1998) P. Moreno, Instituto Valenciano de Investigaciones, Agrarias, Apartado Oficial 46113 Moncada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citrus tristeza virus.
Citrus tristeza virus
                                                                                                                                                                                                                                                                                                                                                                                                            99190444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tristeza virus complete genome, isolate T385.
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NHT Homo sapiens cDNA clone 1031443 3'; (355. .128); 100%
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                                                                                                                                note="ORF1"
                                                                                                                                                                                                                          /virion
                                                                                                                                                                                                                                       organism="Citrus tristeza virus"
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94.4%;
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Pred. No. 2.3e+02;
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LVKLSDYNUNSAALVLALTLTREKREKFLLRTLFDTLLADLRRTASLSEYSKKYPITR
NDIDVVSSRMGIVVSKYLRGSDLERIPL"
13712. 15319
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PTFAVRSSGGDMNLGGRDIDKKLSDKIYEMADFIPGKELNVSSLKEALSJQTDPVKYT
VTHHGMSETISIDQTALEIASVFIRRTIDLITQVKVKSSMPBSQSLKLVVVGGSSYL
PGLLDTLATVPFVSGIVPVEDARTAVARGCALYSECLDGRSKALLIDCITHHLSVTTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORF7"
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/note="ORF5"
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/db_xref="pID:ei375381"
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/rdb_xr
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                                                                                                                                                                                                                                                                                                                     78.18;
                                                                                                                                                                                                                                                       Score 16.4; DB 17;
Pred. No. 2.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                 19259;
                                                                                                                                                                                                                                                              0,
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Search completed: August 18, 1999, 17:17:40 Job time: 3506 sec

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14.4 14.4

68.6 68.6

Enterococcus faeca Human secreted pro

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 1999, 17:18:36 ; Search time 148.09 Seconds (without alignments) 35.479 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-004-395-5 21 1 tgggataaataattggagcgt 21

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database : N\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| 0 44               |                | c 40   |                   | ر<br>م<br>د<br>د |                    | c 35         |          |              |              | 31           | 30      | 29     | 28             | 27     |             | c 25     | 24             | 23     | 22     | 21     | c 20   | 19     | c 18               | 17                 |                    | c 15              |          | 13     | 12     | c 11    | 10     | Q                  |             |                   |        |         |           | ი<br>3 |             |              | No.         | Result |           |
|--------------------|----------------|--------|-------------------|------------------|--------------------|--------------|----------|--------------|--------------|--------------|---------|--------|----------------|--------|-------------|----------|----------------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|-------------------|----------|--------|--------|---------|--------|--------------------|-------------|-------------------|--------|---------|-----------|--------|-------------|--------------|-------------|--------|-----------|
| 14.4               | 14.4           | 4      | ٠.                | - ÷              | 14.8               | ٠.           | .4       | 4            | 4            | 4            | •       | 4      | ٠.             | Ģ      | 5           | 5        | 5              | 5      | 5      | 5      | 5      | 5      | 5                  | 5                  | 5                  | 'n                | 5        | ū      | 5      | 5       | 5      |                    | 5           | 5                 | 5      | 5       | 5         | 5      | 21          | 21           | Score       |        |           |
| 9.9                | . 0            | ٩      | Θ١                | <u>ء</u> م       | ۰.                 | .0           | 0        | 0            | 70.5         |              |         |        | 70.5           | 72.4   | 72.4        | 72.4     | 72.4           | 72.4   | 72.4   | 72.4   |        | 75.2   | 5                  | <u>ب</u>           |                    |                   | <u>ა</u> | 5      | 5      |         | ر<br>د | ٠,                 | 75.2        | ٠.                | ٠,     | 5       | <u>.</u>  | ٠.     | 100.0       | 100.0        | •           | Query  | æ         |
| 13740              | 3467           | 1801   | 2619              | 1801             | 5653               | 13868        | 474      | 1342         | 57           | 12368        | 1228    | 1158   | 1641           | 850    | œ           | 28690    | 735            | 894    | 894    | 831    | 3427   | 1177   | 2462               | 968                | 1780               | 1198              | 773      | 1518   | 1518   | 1197    | 1810   | 1803               | 1829        | 1174              | 1150   | 1199    | 1193      | 1088   | 110000      | 110000       | Length 1    |        |           |
| <b>⊢</b> +         |                |        |                   |                  |                    |              |          |              |              |              |         |        |                |        |             |          |                |        |        |        |        |        |                    |                    |                    |                   |          |        |        |         |        |                    |             |                   |        |         |           |        | _           | r            | : BB        |        |           |
| V74365             |                | X16778 | V74173            | V16947           | X12989             | V74484       | V75233   | V62449       | V07655       | V31206       | T84170  | T34672 | T34671         | X14060 | X14361      | X13075   | V25016         | V24748 | T68071 | T67692 | Q56733 | X20333 | x20299             | X20345             | X14142             | V36343            | V20402   | V20910 | V20911 | T85615  | T45043 | T45042             | T45041      | 051020            | 034840 | 014736  | 004644    | N90126 | 0248        | x20248_01    | ID          |        | SUMMARIES |
| Staphylococcus aur | ronectin-bindi | bisco  | Human huBUR3 gene | ccus             | Enterococcus faeca | taphylococcu | lococcus | n neurotensi | DNA encoding | coli J96 pat | ncoding | t pro  | uclear inclusi | pylori | pylori GHPO | terococc | pylori cytopla | pylori | •      | lori   | c      |        | Borrelia burgdorfe | Borrella burgdorfe | H. pylori GHPO 358 | cDNA encoding the |          |        | ру1о   | of<br>C | CP2    | Helicobacter CP2 A | obacter CP2 | Human FreeT alpha |        | crepsil | les alpha | a hum  | inuation (3 | ntinuation ( | Description |        |           |

| Qy 1 tgggataaataattggagcgt 21 | Query Match 100.0%; Score 21; DB 1; Length 110000;<br>Best Local Similarity 100.0%; Pred. No. 0.2;<br>Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | X20248_02/c  X20248_02/c  Continuation (3 of 10) of X20248 from base 200001 (Borrelia burgdorferi polynucleotid WP Sequence split into 10 fragments LCUS X20248 Accession X20248  WP X20248_00 1 10000  WP X20248_01 100001 210000  WP X20248_02 200001 310000  WP X20248_03 300001 410000  WP X20248_04 400001 510000  WP X20248_05 500001 510000  WP X20248_05 500001 710000  WP X20248_06 600001 710000  WP X20248_08 800001 910000  WP X20248_09 900001 910715 | Qy 1 tgggataaataattggagcgt 21<br> | <pre>Query Match</pre> | RESULT 1  x20248_01/c Continuation (2 of 10) of x20248 from base 100001 (Borrelia burgdorferi polynucleotid Pragments LOCUS x20248 Accession x20248  WP Sequence split into 10 fragments LOCUS x20248 Accession x20248  WP x20248_00  WP x20248_01  WP x20248_02  WP x20248_03  WP x20248_03  WP x20248_04  WP x20248_05  WP x20248_05  WP x20248_05  WP x20248_05  WP x20248_06  WP x20248_06  WP x20248_06  WP x20248_08  WP x20248_08  WP x20248_09  WP x20248_ | ALIGNMENTS |
|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|

|                                                | Qy 1 tgggataaataattggagcgt 21 | Matches 21; Conservative 0; Mism |
|------------------------------------------------|-------------------------------|----------------------------------|
| IGE receptor al or alpha subunit drugs; human. | τ 88<br>4                     | 0; Mismatches                    |
| pha:<br>; tr                                   |                               | 0,                               |
| subunit<br>eats                                |                               | Indels                           |
|                                                |                               | 0;                               |
|                                                |                               | Gaps                             |

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RESULT
Q14736/c
ID Q147
AC Q147
DT 03-F
DE Huma
KW Immu
OS Homo
FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q0464/c
ID 644/c
ID 2046
AC Q046
AC Q046
AC Q046
AC WW high
KW high
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PP 18-C
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Best Local S
Matches 17
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01-DEC-1987; US-127214.
(HARD) Harvard College.
Straganian R, Shimizu A, I
WPI: 89-192698/26.
                                            Q14736 standard; cDNF
Q14736;
Q14736;
O3-FEB-1992 (first e
Human Fc(epsilon)RI a
Immunoglobulin; recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences for subunit peptides of high affinity IgE receptor - and derived polypeptides, for therapy and diagnosis of allergies, and studies of IgE receptor interaction Disclosure; p; English.

The high affinity receptor is a tetrameric complex consisting of 2 gamma subunits and one each of subunits alpha and beta. It is expressed on mast cells and is involved in the allergic response. COS-7 cells cotransfected with cDNA for all 3 intact subunit types (derived from rat basophilic leukaemia cells) express receptor on their surfaces. Detailed study of the receptors is now possible. Sequence 1193 BP; 384 A; 241 C; 247 G; 321 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA encoding IgE receptor alpha-subunit - used to treat all Disclosure; fig 4; 18pp; English.

CDNA sequence encoding immunoglobulin E receptor alpha subunit of human mast cell IgE surface receptor (see corres used to produce antibodies which can diagnose IgE receptor measure and treat allergies, and design non-peptide drugs. Sequence 1088 BP; 347 A; 216 C; 229 G; 296 T;
  Homo
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-1989; U04628.
18-OCT-1988; US-259065.
(USDC) US Sec of Commerce
Kinet JP, Metzger H;
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P-PSDB; R05025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encodes alpha subunit of human highigh affinity IgE receptor; alpha human; allergic response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q04644 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9004640-A.
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                                            n)RI alpha cDNA.
receptor; high affinity
                                                                                                                                           cDNA; 1199
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or; alpha subunit of
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01-DEC-1992.
02-JUL-1990; 230085.
24-FEB-1988; US-160457.
02-JUL-1990; US-547892.
(USSH ) US DEPT HEALTH &
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15-OCT-1991.
14-DEC-1990; 151091.
14-DEC-1990; US-626704.
(USSH) NAT INST OF HEAL
Kinet JP, Metzger H;
WPI; 91-346755/47.
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18-ARR-1996 (first entry)
07-MAY-1993 (first entry)
Human high affinity IgE receptor alpha subunit
Allergic response; antagonist; drug screening;
reaction; diagnosis; therapy; FCERI; ss.
Novel DNA encoding alpha sub-unit of human high affinity IgE receptor - useful as antagonist to prevent allergic response, reagent in drug screening and for antibody generation Disclosure; Fig 1; 34pp; English.

The sequence is that of the gene encoding the human IgE high receptor alpha subunit (FCERI). It may be used to synthesise human FCERI alpha subunit or to synthesise cDNA sequences to construct DNA probes useful in diagnostic assays.

Sequence 1150 BP; 373 A; 237 C; 227 G; 310 T;
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Disclosure; Fig 1: 58pp; English.

A lambda gtl1 library was prepared from poly-A RNA isolated fr KUB12 cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha cDNA corresponding to nucleotides 119-781.

Positive Clones were subcloned and sequenced.

Sequence 1199 BP; 390 A; 241 C; 247 G; 321 T;
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745
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28-OCT-1993.
16-APR-1993; U03419.
16-APR-1992; US-869933.
(USSH ) US DEPT HEALTH &
Kinet JP;
                                                                                                                                             T45041;
                                                                                               24-FEB-1997 (first entry)
Helicobacter CP2 antigen structural gene.
CP2; antigen; vaccine; diagnosis; gastritis;
Helicobacter pylori strain ATCC 43504.
                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 154pp; English.

The sequence is that of the human FCRI alpha subunit, isolated by using first strand reverse transcriptase from human basophils by the gene and its prod. can be used to identify human beta subuit FCRI inhibitors (immunoglobulin E receptor) which inhibit the binding of IgE to its receptor and inhibit the aggragation functiof the receptor or the signal transducing function related to allergic response. Such inhibitors can be used for the treatment prevention of allergic disease.

See also 051021-4.
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IgE; immunoglogulin E receptor; be aggregation; signal transduction;
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complement (18. .
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complement (97. .
/*tag= c
/note= "forward F
364. .385
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107. .881
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89
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89
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ransduction; diagnosis; antagonist;
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                                        amplification"
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           detection
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                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in the production of vaccines Claim 3; Page 16-18; 29pp; English.

A structural gene (T45041) of Helicobacter pylori ATCC 43504 codes for the CP2 antigen (W06481) useful in vaccine produ. Genomic for the CP2 antigen (W06481) useful in vaccine produ. Genomic fragments of H. pylori DNA were inserted into vector pBluescript, and E. coli JM109 transformants were screened using a probe based on the N-terminal sequence of CP2. PCR primers (T45048-49) based on the N-terminal sequence of CP2. PCR primers (T45048-49) based on isolated clones were then used to amplify the structural gene. The gene sequence differs slightly from those of CP2 genes (see also T45042 and T45043) obtd. by PCR amplification. CP2 genes can be used to produce recombinant CP2 in transformed host cells, or to design primers (see also T45044-47) useful in the specific detection of H. pylori.

Sequence 1829 BP; 589 A; 337 C; 409 G; 494 T;
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Matches 17
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T45042;
24-FEB-1997
EP-745674-A2.
04-DEC-1996.
30-MAY-1996;
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WPI; 97-013697/02.
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05-APR-1996; JP-083512.
(WAKP ) WAKO PURE CHEM IND
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17; Conserv
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PI Hirayasu K, Kawabata T, Sugiyama T, Tanaka T;

PP Hyp: 97-013697/02.

PP PSDB: W06482.

PT corresponding DNA, useful as reagents for detecting H. pylori and in the production of vaccines Claim 3; Page 18-20, 29pp; English.

PS Claim 3; Page 18-20, 29pp; English.

CLaim 3; Page 18-20, 29pp; English.

CLaim 3; Page 18-20, 29pp; English.

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05-APR-1996;
(WAKP ) WAKO
Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori are the production of vaccines Claim 3; Page 21-23; 29pp; English.

A structural gene (T45043), designated CP2-PCR2, codes for the Cantigen (W06483) of a clinical isolate of Helicobacter pylori obtains a patient with chronic gastritis. It was produced by PCR amplification using primers (see also T45048-49) based on the CP2-PCR2
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30-MAY 1996; 108637.
02-JUN-1995; JP-136564.
05-APR-1996; JP-083512.
(WAKP ) WAKO PURE CHEM IND
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D PURE CHEM IND
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Claim 1; Fig 1A-B; 15pp; English.
This cDNA sequence encodes the alpha subunit of the human high affinity
receptor for IgE (FCERI). FCERI is found exclusively on mast cells,
receptor for IgE (FCERI). FCERI is found exclusively on mast cells,
basophils and related cells. Aggregation of IgE occupied FCERI by antig
triggers both the release of of preformed mediators such as histamine a
serotonin, as well as stimulating the synthesis of leukotrienes. It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha subunit of human high affinity receptor for IgE alpha subunit; human high affinity receptor; IgE; FCER, preformed mediator; histamine; serotonin; leukotriene; allergic condition; therapy; allergic response; drug so DNA probe; diagnostic assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence differs slightly from that of CP2 and from clone CP2-PCR: (T45042) obtd. by PCR amplification of ATCC 43501 DNA. Isolation of CP2 genes allows the mass prodn. of CP2 protein in transformed host cells for use in vaccines. The genes can also be used to design primers (see also T45044-47) useful in the specific detection of H. pylori.

Sequence 1810 BP; 575 A; 323 C; 410 G; 502 T;
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                                                                                                           the release of these mediators that results in an allergic condition. The DNA can be used to produce the human FCERI alpha polypeptides which can be used for therapy or to prevent allergic responses, in drug screening assays or for monitoring IgE levels in patients. The DNA can also be use to produce DNA probes useful in diagnostic assays.

Sequence 1197 BP; 389 A; 242 C; 245 G; 321 T;
                                                                                                                                                                                                                                                                                                       DNA encoding alpha sub-unit of high affinity receptor immunoglobulin E - used for producing polypeptide(s) used for therapy or to prevent allergic responses or
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(USSH ) US DEPT HEALTH & HUMAN
Kinet JP, Kochan JP;
WPI: 97-332052/30.
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17-JUN-1997.
24-FEB-1988; 160457.
24-FEB-1988; US-160457.
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Matches 17
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19-FEB-1998.
14-AUG-1997; AUOS15.
15-AUG-1996; US-695987.
(CSLC-) CSL LTD.
(CSLC-) UNIV NEW SOUTH WALES.
DOIDGE CV, HAZELI SL, Lee A, R
WPI; 98-159544/14.
P-PSDB; W52810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Helicobacter catalase nucleic acid - used to develop products for the treatment or prevention of Helicobacter infection, particularly H. pylori gastroduodenal disease Claim 29; Page 33-37; 46pp; English.

The Helicobacter pylori catalase gene encodes a protein of 58650 Da. The protein, gene sequence and products, such as an immunogenic fragmer can be used for the treatment or prevention of Helicobacter infection, particularly H. pylori infections which cause gastroduodenal disease. They can also be used for the detection and diagnosis of Helicobacter
               New isolated Helicobacter catalase nucleic acid - used to develop products for the treatment or prevention of Helicobacter infection, particularly H. pylori gastroduodenal disease Claim 29; Page 31-33; 46pp; English.

The Helicobacter pylori catalase gene encodes a protein of 58650 Da.

The protein, gene sequence and products, such as an immunogenic fragment, can be used for the treatment or prevention of Helicobacter infection,
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(UYNE-) UNIV NEW SOUTH WALES.
DOIDGING CV, Hazell SL, Lee A,
WPI; 98-159544/14.
P-PSDB: W54146.
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Helicobacter pylori isolate RUI catalase gene.
Treatment; prevention; gastroduodenal disease;
Helicobacter pylori.
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V20911;
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15-AUG-1996; US-695987.
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on; gastroduodenal disease; detection;
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                                                                                                                                                                                                                          New fusion polypeptide for, e.g. diagnosing allergies - comprises immunoglobulin E-binding domain fused to human serum albumin Disclosure; Page 56; 77pp; English.

C fils nucleotide sequence codes the dominant form of full-length native human IgE receptor Fc-epsilon RI alpha chain (see W48094).

A claimed fusion protein (FP) comprises an IgE binding domain fused to at least one human serum albumin (HSA) component (see W38095).

C (see W48096) comprising HSA fused, at each of its N- and C-termini, to the extracellular domain (i.e. mature protein) of Fc-epsilon RI to the extracellular domain (i.e. mature protein) of Fc-epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP; a vector; a process for preparing the FP; a method of performing gene therapy in humans that comprises removing somatic cells from a polynucleotide that encodes the FP, and reintroducing the modified cells into the patient; so that the FP is expressed by the cells of the patient; and use of the FP in an in vitro diagnostic assay to determine the level of IgE or auto-antibodies to Fc epsilon RI in a sample. The products can be used in the heavent on Education RI in a
                                           Query Match
Best Local S
Matches 17
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                                                                                                                   sample. The products can be used in the prevention and/or treatment of IgE-mediated allergic diseases and related disorders such as atopic dermatitis, atopic asthma, chronic urticaria, hayfever and eczema. Compared with using IgE binding domain alone, the FP has a longer serum life, and thus greater activity, without a loss of ability to bind serum IgE or circulating auto-antibodies. Sequence 773 BP; 220 A; 173 C; 176 G; 204 T;
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Fc-epsilon RI alpha chain; IGE receptor; human serum albumin;
fusion protein; allergy; atopic dermatitis; asthma; urticaria;
hay fever; eczema; anaphylaxis; gene therapy; diagnosis;
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Digan ME, Gram H, La
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transgenic animal; ds.
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26-JUL-1996;
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V36343/s

V36343 standard; cDNA; 1198 BP.

AC V36343 standard; cDNA; 1198 BP.

AC V36343 standard; cDNA; 1198 BP.

AC V36343 standard; cDNA; 1198 BP.

AC V36343 standard; cDNA; 1198 BP.

AC V36343;

DT CONCT-1998 (first entry)

DE cDNA encoding the alpha chain of a Fc epsilon receptor.

Alpha chain; human; Fc epsilon receptor; canine; equine; feline;

KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;

KW Alpha chain; human; Fc epsilon receptor; disgnose; allergy; atopic disease;

KW immunoglobulin E; IGE; detection; ds.

Alpha chain; human; Fc epsilon; ds.

OS Homo sapiens.

Location/Qualifiers

FT KBY

MY MY 1998:

LOCATION/QUALIFIERS

FT CDS

FT CDS

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PA (H5SK-) HESKA CORP.

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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of non-human immunoglobulin E - by complex formation with human Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic disease
Claim 11: Pages 36-37; 70pp; English.
The present sequence encodes the alpha chain of the human Fc epsilon receptor. Detection of canine, equine or feline immunoglobulin E (IgE) comprises reacting isolated human Fc epsilon receptor with the test sample and detecting formation of a IgE-receptor complex. Detection of IgE seceptor internal parasitic infections or B cell neoplasia, and for measuring effect of treatments. Most particularly flea allergy in dogs and cats is detected, and also heartworm infection.

Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T;
                                                                                                                                                                                                          733
                                                                                                                                                                                                  75.2%;
                                                                                                                                                                                                          715
                                                                                                                                                                                                                                                                                                                                                              ; Score 15.8; Di
; Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1198;
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    US-09-004-395-5
21
1 tgggataaataattggagcgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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| 58:        | 7      | 56:        | 55:        | 54:        |
|------------|--------|------------|------------|------------|
| em_est26:* | est25: | em_est24:* | em_est23:* | em_est22:* |
|            |        |            |            |            |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|             |              | •       | ,                | n              | a            | ი               |               | ი               | ი               |              | a                |               | a               |                 |                 |                | o              | ი              |               | ი           | ი             |               | ი             |              |               |                | o              | ი                | O              | o i              | ი (              | ი               |                 |                 |                     |                 | C                | G                | a               | ဂ               | O                | O             | ი          | ი              | Resul<br>No    |
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| 4           |              | - (     | 2                | 42             | 41           | 40              | 39            | 8               | 37              | 36           | i U              | 4             | . (L            | 2               | 31              | 30             | 29             | 28             | 27            | 26          | 25            | 24            | 23            | 22           | 21            | 20             | 19             | 18               | 17             | 16               | 15               | 14              | 13              | 12              | 1 7                 | 10              | οa               | ۰ -              | <b>3</b> 0      | 'n              | 4                | ω             | N          | <b>–</b>       | , t            |
| 14.8        | ۰            | ١.      | л                | 5              | ŗ            | ŗ               | 5             | ŗ               | ŗ               | ŗ            | Ü                | ij            | Ü               | ij              | Ü               | ij             | ŗ              | ŗ              | ŗ             | 5           | ŗ             | ŗ             | Ģ             | 5            | 5             | ū              | 5              | 'n               | Ü              | 5                | J ا              | 5               | S               | 5               | л:                  | л:              | ٠.               | ١,٠              | י פ             | 16.2            | ņ                | 9             | 5          | 7              | Score          |
|             | ٠            | 7:      | ٥                | N              |              |                 |               | Ņ               | N               |              | N                | Ņ             |                 |                 |                 | 72.4           |                | 72.4           | 72.4          | 72.4        | 72.4          | 72.4          |               |              | Ņ             | 2              | ω<br>·         | ω.               |                | w.               | ω.               | ω:              | w               | ω :             | •                   | ñ u             |                  | ij               | 7.              | 77.1            | ٠                | •             | 7          | 82.9           | Query<br>Match |
| 7           |              | пι      | л                | Ų.             | 7            | w               | N             | 0               | 4               | •            | •                | Š             | α               | v               | 0               | 0              | œ              | 4              | 0             | S           | 4             | 9             | 4             | Ν            | ū             | 9              | ū              | -                | 479            | wι               | ₽,               | ω.              | 71              | N               | л                   | - 4             | 3/0              | ıυ               | 3 00            | 417             | •                | ·w            | w          | w              | Length         |
| 50          | ť            | 5 1     | 2                | 51             | 50           | 50              | 45            | 44              | 44              | 42           | 0                | 40            | 40              | 39              | S.              | ω              | 34             | 34             | 29            | 25          | 24            | 23            | 22            | 22           | 20            | 20             | 51             | 50               | 50             | 8                | 5                | <u>۵</u>        | ω (             | ω e             | <u>بر</u>           | n (             | 4 7              | 5                | 47              | 6               | 6                | 40            | 27         | 25             | BB             |
| AU066662    | CCTCA        | 111111  | CW01185          | 173382         | 24           | 1379            | 4133          | 26264           | 25144           | 15           | 500              | C82644        | 7672            | 94              | 1836            | 847            | 8168           | 454            | 8682          | 431         | 8             | 80            | 89            | 445          | 2332          | 18656          | 72222          | V03048           | 1688           | I54536           | I35078           | 21856           | 57435           | 57429           | 2110                | 2000            | 101              | 22002            | 52287           | 146             | 6066             | 96286         | 497        | 109            | ID             |
| 662 AU06666 | TO94 EST2407 | 1011011 | 1047001 0000 500 | 733829 ck34f04 | 6241 AV04624 | 043793 AV043793 | 1339 qx90h10. | 262642 qk34f04. | 251447 qu74g06. | I150563 qf36 | 83500 C83500 rab | 44 C82644 rab | A976721 oq06e04 | 894898 nz47hll. | 1836 C51836 Yuj | 8476 C38476 Yu | 81687 zv45c03. | 54469 zw28g07. | 86829 zp73h10 | 431 zb77e11 | 607 yv22c12.s | 807 y142c07.r | 680 yj74f09.r | 450 yl25d03. | 23327 5c07g04 | 656 SC01A07-T7 | 722228 fd20f09 | V030487 AV030487 | 1688192 wc87a0 | 1545362 fb74c12. | 1350781 qq21d04. | 218562 ah19e01. | 574359 nf46a09. | A574291 nf45a09 | 119 % 648 8 8 9 60. | 1605766 +130608 | 1511010 01-K-C2p | AZZ60Z5 nCUYEIU. | 522878 sa74h08. | 1461277 sa60h09 | 1460669 sa71g09. | 962861 L30-48 | 7 C06497 H | 1091 HUM129E12 | Description    |

#### ALIGNMENTS

| VERSION                         | ACCESSION                     | DEFINITION | Locus                         | D81091/c | RESULT 1 |
|---------------------------------|-------------------------------|------------|-------------------------------|----------|----------|
| 91178968<br>D81091.1 GI:1178968 | GEN-129E12 5', mkNA sequence. | -          | D81091 308 bp mRNA EST 09-FEB |          |          |
|                                 |                               | A clone    | 1996                          |          |          |

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TITLE
JOURNAL
COMMENT
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C06497/c
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57 TGGGATAAATATYTGGAGAGT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 kagasuno Kawauchi-cho, T Tel: 0886-65-2888 Fax: 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                          C06497
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similar to cy
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C06497.1
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1 (bases 1 to 308)

Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagarokuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.

Fujiwara et al. (1995)
                                                                                                                                               Institute for Molecular and Cellular Regulation, 3-39-15 Showa-machi, Maebashi Gunma 371, Japan Tel: 272-20-8856 Fax: 272-20-8896
                                                                                                                                                                                                                                      Unpublished (1995)
On Apr 14, 1993 this sequence version replaced g1:315339
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                              Contact: Jun Takeda
                                                                                                                                                                                                                                                                                        Takeda, J.
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                                                                                                                                                                                                                                                                      pancreatic islet ESTs
                                                                                                               jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
/clone_lib="Human pancreatic islet"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_l: Eco RI;
/r mRNA was prepared from normal adult human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human fetal brain (TFujiwara)"
/dev_stage="fetal"
/note="organ: brain"
65 c 55 g 72 t 25 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                   /clone="hbc5859"
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1. No. 1.1e+02;
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sapiens cDNA clone hbc5859
mRNA sequence.
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An expressed sequence tag data
An expressed sequence tag data
Mesembryanthemum crystallinum
Unpublished (1997)
On Jan 14, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biochemistry and Molecular Biology Oklahoma State University
350 Noble Research Center, Stillwater, OK 74078-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae;
                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 280 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: T7
BACKWARD: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 405-744-6207
Fax: 405-744-7799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cushman JC
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                                                                                                                                                                   /organism="Mesembryanthemum crystallinum"
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/clone=lib="Ice plant Lambda Uni-Zap XR explibrary, 30 hours NaCl treatment"
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/dev_stage="Six week old"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript
EcoRI; Site_2: XhoI"
2 a 100 c 120 g 137 t
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118 c 131 g 113 t 1 others
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85.7%;
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Pred. No. 3.5e+02;
0; Mismatches 3
                                                     Score 16.2; DB 4v,
Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189594.
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Fax: 314 286 1810
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Seq primer: -40RP from G1bco
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             /tissue_type="root"
//lab_host="xil0-Gold"
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/clone="GENOME SYSTEMS CLONE
/clone_lib="Gm-cl004"
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colonies appear to contain recombinant
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                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3247126
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Fax: 314 286 1810
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Seq primer: -40RP from Gibco.
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/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated of
                                                                                  /tissue_type="root"
/lab_host="XL10-Gold"
                                                                                                                                        /clone="GENOME SYSTEMS CLONE
/clone_lib="Gm-c1004"
                                                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
/map="14q24.3"
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Pred. No. 3.7e+02;
0; Mismatches 3;
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Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T.,
Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
                               Washington University School of Medicine
                                                                       Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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Shoemaker, R., Brine
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                                                                                                                               On Mar 10, 1998 this sequence version replaced gi:2949473
                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                     Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.1%;
85.7%;
                                                                                                                                                                                                                                                                                   Briner, D., Marra, M., Hillier, L., Kucaba, T.,
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                                   Louis, MO 63108, USP
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                                                                                                                                                                                                                                                                                                        sequence.
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                                                                                                                                                                                                                                                                                                                                                                    nc09e10.sl NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007658, mRNA
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                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
                                                                                                                                           Homo sapiens
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EST.
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1 (Dases 1 to 554)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhOI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA synthesis Kit (catalog #200401) was used to synthesize the cDNA. First strand synthesis was performed with 5-methyl cCDNA. First strand synthesis was performed with 5-methyl CDNA, hence the ligated CDNA is hemmethylated. Stratagene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' second-strand synthesis, the cDNA ends were 'polished'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520-523-7500, email: paul.keim@nau.edu,
virginia.coryell@nau.edu"
a 99 c 119 g 132 t 2 othe
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/lab_host="XL10-Gold"
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/clone_lib="Gm-c1004"
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/db_xref="taxon:3847"
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85.7%;
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RESULT 8
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cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 370)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                              UI-R-C:
AI51101
                                                                                                                                                                                                                                                                                                                                             AI511010 370 bp mRNA EST 15-MAR-1999
UI-R-C2p-ny-h-06-0-UI.sl UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-ny-h-06-0-UI 3', mRNA sequence.
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On Sep 12, 1996 this sequence version replaced gi:1316602.
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                                                                discovery
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AI511010.1 GI:4416709
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                                             Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                 Norway rat.
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                                                                                        Normalization and subtraction: two approaches to
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Jun 22, 1998 this sequence version replaced gi:3246630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of For applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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/db_xref="taxon:9606"
/map="884810; 9; 9922.2-922.32; 9922.32-931.2"
/cione="INAGE:1007658"
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/lab_host="DH10B"
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/sex="Male"
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89.5%;
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Pred. No. 5.9e+02;
0; Mismatches 2;
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                                                                                           facilitate gene
                                                                                                                                                              Mammalia;
Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGATAAATACTTGGAGAG 149
                                                                                                                                                                                                               A1676097 446 bp mRNA EST 19-MAY-1999 wC05c12.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314294 3' similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
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                                                                               Homo sapiens
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                                                                                                         human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /notes "vector: pr773b-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"
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/lab_host="DH10B (Life Technologies)"
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/clone_11b="UI-R-C2p"
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/db_xref="taxon:10116"
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Pred. No. 5.8e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                              AI685796 540 bp mRNA EST 27-MAY-1999 tu20g08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251646 3' similar to gb:X06948 HIGH AFFINITY IMMUNOCLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conser
                                            Tumor Gene Index
Unpublished (1997)
On Feb 18, 1999 this sequence version replaced g1:4314787
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On Dec 20, 1995 this sequence version replaced gi:1133931
  Contact:
                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 540)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

74 c
75 g
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Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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Pred. No. 5.5e+02;
0; Mismatches 2;
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 554)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Kucaba, T., Lacy, M., Le, M., Le, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Parange, C., Riikin, L., Mardis, E., Woore, B., Morris, M., Parsons, J., Prange, C., Riikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M92119 554 bp mRNA EST 02-FEB-19 zh48a09.rl Soares_fettal_liver_spleen_lNFLS_S1 Homo sapiens clone IMAGE:415288 5' similar to gb:X75755_rna2 SPLICING F7 SC35 (HUMAN);, mRNA sequence.
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Location/Qualifiers
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
    On Oct 18,
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with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

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/db_xref="taxon:9606"
/clone="IMAGE:2251646"
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    1995 this
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89.5%;
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sequence version replaced gi:1023832.
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Pred. No. 5.2e+02;
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SPLICING FACTOR
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Contact: Wilson

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Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Eduencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                        rel: (301) 496-1550
Email: Robert C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                          암
                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA574291.1
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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/db_xref="GDB:1323758"
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Pred. No. 7.9e+02;
D; Mismatches 2;
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www-bio.llnl.gov/bbrp/image/image.html

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tgggataaataattgga 17
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA574359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA574359 375 bp mRNA EST 29-AUG-1997 nf46a09.sl NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:916792, mRNA
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                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 375)
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www-bio.llnl.gov/bbrp/1mage/1mage.html
                                                                                                                                                                                                                                                        On Apr 14, 1993 this sequence version replaced g1:693408
                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.n1h.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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Similarity 94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="45 years old"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 8.5e+02;
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AI218562/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI218562 438 bp mRNA EST 17-M-qh19e01.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone mAGE: 1845144 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 th
                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tenail: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 438)
                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                             High quality sequence stop: 422.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/map="1, 2q, 14; 1, 2q, 14;
/clone="IMAGE:1845144"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                         Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                          this sequence version replaced gi:2150572
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Pred. No. 8.8e+02;
0; Mismatches 1;
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AI350781/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 416)
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-89479. "
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                                                                                                                                                                                                                                                                                                                                                  /Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:1933159"
/clone=lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart,
pregnant uterus"
pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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### ALIGNMENTS

| MEDLINE<br>REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL                                                                                                                                                 | AUTHORS<br>TITLE<br>JOURNAL                                                                                                                                           | SOURCE<br>ORGANISM<br>REFERENCE                                                                                                                    | ACCESSION<br>NID<br>VERSION<br>KEYWORDS                                                                       | RESULT 1 BBCHEAGEN/c LOCUS DEFINITION                            |
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| 98438936<br>2 (bases 1 to 332)<br>Old, I.G.<br>Direct Submission<br>Submitted (03-0CT-1995) I.G. Old, Institut Pasteur, Bacteriology &<br>Mycology, 28 rue du Dr Roux, 75724 Paris cedex 15, FRANCE | Trueba,G.A., Old,I.G., Saint Girons,I. and Johnson,R.C. A cheA cheW operon in Borrelia burgdorferi, the agent of Lyme disease Res. Microbiol. 148 (3), 191-200 (1997) | Lyme disease spirochete.  Borrella burgdorferi Bacterla; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group. 1 (bases 1 to 332) | X91907<br>g1019753<br>X91907.1 GI:1019753<br>CheA gene; cheA protein; chemotactic response protein; histidine | BBCHEAGEN 332 bp DNA BCT 20-JAN-1998<br>B.burgdorferi cheA gene. |

Result No.

Query Score Match Length DB ID

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332 1 BBCHEAGEN

Description X91907 B.burgdorfe

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1 (bases 1 to 13271)
Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A.
Fraser,C.R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,
Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D.,
Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,
Salzberg,S., Hanson,M., van-Vugt,R., Palmer, N., Adams,M.D.,
Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,
Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Hor
Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi (section 54 AE001168 AE000783 g2688598
                   98065943
                                Nature 390 (6660), 580-586 (1997)
                                                   burgdorferi
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/db_xref="PID:g1019755"
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                          Clayton, R.A.,
                                                                                            McDonald,L.,
,M.D., Horst,K.,
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                                                                                                           /gene="BB0670"
3769. .5169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0669"
1168. .3762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="BB0669"
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                                                                                                                                             .5169
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                                                             881576 percent similarity; pu
                  chemotaxis
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Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.,-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K., Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
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Submitted (12-DEC-1997) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                         /translation="MEILDLENEELLGVFFEEAQNIVDILEENIMSLEDDPNNSDTID
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EGLGIGQKVLRISVVFNSNSSEVENSGLKIFNILKNLGSVLHTIPKYEQIIEDKFLK
RVDYYLLIYSDLEGVKKSLDSLWLIESTLYDEFENVKEELKKLADEELKOVDLDSNFVLN
DNFDFTEDELSDLLEEVENQKLFKVRLDFVKNDMATISGCAMLQALKSLGKIFKSIP
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DEAPFKENKNIKNSPLSVHLIRIDSKKIDYILNUSSAVISKFKEEKALKDISELF
NFNTYYDYOGSEFORNFLIDLKIVFKDAGLFLEDEIESHINSLMSFKKEKALKDISELF
NFNTYTYDYOGSEFORNFLIDLKIVFKDAGLFLEDEIESHINSLMSFKKEKALKDISELF
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NFTRYDYOGSFORNFLISNITSHESVLKTRMLPISNIFSRFTRYVRDLSKKLUKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLKMEGEETELDKSVIDDLYDPLMHCVRNSMDHGLETVEERVKRGKSKAGTIILRAKN
EGNVISIEIEDDGIGIDPKVIRRKLIEKGTIKEDAIYSDFELINLIFAPGFSTAVQVT
DLSGRGVGLDVVKKSIEKLNGTILVESEIGLGTIFKIKLPLTLVIIQGLLVKSGSETY
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GLIDNIKTMKEIKVSVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPN
YIPNISSRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKEQNFIFYVKDLRVLYDKLSV
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AELARDPSSTRLDLINYYDIYYYSGASGIYKPEDMYVDLGINNMSVLLFPSARLQAYYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/trans1_table=11
/product="Chemotaxis histidine kinase (cheA-2)"
/protein_id="AAC67024.1"
/db_xref="PID:92688607"
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VVNTSNMKIAIVVDSILGEEDFVVKPIKDKFSSSAGIVGATTLGNGKVVLIIDVFKLF
                                                   VIPLNNVLETHRITEHDIKLLENYHEVYNLRDEVISVLRLDKLFNITRDDSLIEKFL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIDSDIDSESVFKVYETSGTESLRKLKAHETFKRVLKLREKISMPEGSFQNFVEKIES
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identified by sequence similarity; putative"
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nt identity: putative"

98.93;

protein (cheW-3)"

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/gene-
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QVKEIRKSSNFTYPDNAKKYNAGLDNLAGEIFFIDLIRLIKMFLEFNKKDIEDIMYLKN
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FNYGEEKLLKPGQNFVEKSDFVSDCDNLDILENSKNDFSNKVSSKNDGNNENSTLN
TAAFHLENIKKHLKYSFNASLVNDVFLEKVGYVENMYDTDXLPCDSFLNEFYSKSSG
NLWGADCLEEFKNEIVESFNSHUNLNSIFNVLEIGCGSGKETMALANALSEYYVKPF
KLTAIDNDLSKYVETSRLVFSESSIGISSIYSRNSFEQSFGYYKFKSEILSHVLDEYS
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complement(6699. .7745)
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FTSEGENIIDTAADGEEAVIKKKNHYENIDIVTLDITMFKMDGITCLSNIMEFDKNAR
VIMISALGREQLVKDCLIKGAKTFIVKPLDRAKVLQRVMSVFVK"
complement(6187. .6702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="BB0672"
5706. .6146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC67022.i"
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/db_xref="pID:92688610"
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                                                                                                                                                                                                                                                                                                                    complement(6699.
                                                                                                                                                                                                                                                                                                                                           FLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNITYFLKNLDK
ISNEMIFFPRE"
                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
/protein_id="AAC67020.1"
/db_xref="PID:92688603"
/db_xref="GI:2688603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="BB0673"
/note="similar to GP:1408275 percent identity:
identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="chemotaxis response regulator (chey-3)"
/protein_id="AAC67021.1"
/db_xref="PID:92688604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIKEKSTKYFNLYRKV"
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TILNPIMLSLFKLRFLRLLRFNDLI1EIYYNSKEKNLILIAFARTFSMSLLIPFTFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GP:1408274 percent identity: 97.95;
identified by sequence similarity; putative"
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identified by sequence similarity; putative"
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                                                                                                                                                                                                                          /note="hypothetical protein; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=:
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MEDLINE
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AUTHORS
TITLE
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AUTHORS
TITLE
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SOURCE
ORGANISM
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Best Local
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/gene="cheA"
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gene

gene CDS

Sgo

gene CDS

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Submitted (12-JUN-1995) Gabriel A. Trueba, Microbiology, University of Minnesota, 420 Delaware Street S.E., Minneapolis, MN 55455, USA On Dec 12, 1995 this sequence version replaced gi:984522.
                                                                                                                                                                                                                                                                                                                                                                                  burgdorferi group.
1 (bases 1 to 2700)
Trueba, G.A., Old, I.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyme disease spirochete
Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BBU28962 2700 bp DNA BCT Borrelia burgdorferi histidine kinase (cheA) gene,
                                                                                                                                                                                                                                        Trueba, G.A. and Johnson, R.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                cheA cheW operon in Borrelia burgdorferi,
                                                                                                                                                                                                                                                                                 (bases 1 to 2700)
                                                                                                                                                                                                                                                                                                                         Microbiol. 148 (3), 191-200 (1997)
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/gene="cheA"
95. .2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNTKPYFPYLYHYLFNHESIKSLSAIEKEIEILNYLKENKKTIA
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KNYIKILLLLKYLYIKYCFEKGIELTTKNIESTSKAISNDTDFLDEKTAKLIIESFFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSKIVNSIPEKQEFNIIKNISIINEKAYIKEKYPFILIIKEKDDIIYSKSDEIFV
YYSPSEYRVIEMEKTKEYIDKYLQRKSDSILGIFLFTLFASFTIFLMNFYKFFKASFL
NPILLMTKILODPLEYRKIQIPFTLSEEKYYELAKSFNNLLLKEKLNSKRKSKIPLEI
EKYKKIINKNOEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L42023 SP:P44755 PID:1004013 PID:1222502 PID:1204815 percent identity: 25.58; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8599. .9261)
/gene="BB0676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein; identified
putative"
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/gene="BB0675"
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                                                                                                      /organism="Borrelia burgdorferi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8599. .9261)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="B. burgdorferi
/protein_id="AAC67026.1"
/db_xref="PID:g2688609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="BB0675"
                                                                 /db_xref="taxon:139"
                                                                                         /strain="CT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:1113814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="BB0676"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spirochaetales; Spirochaetaceae; Borrelia;
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MEDLINE
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AUTHORS
TITLE
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BBU62900/c
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Matches 21
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1 (bases 1 to 1655)

Ge,Y. and Charon,N.W.
An unexpected flam homolog is present and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BBU62900 1655 bp DNA BCT 1:
Borrelia burgdorferi flagellar filament outsheath pu
gene, complete cds, and chemotaxis histidine kinase
                                                                                                                                                                                                         Submitted (03-JUL-1996) Yigong Ge, Microbiology, HSCN, Morgantown, WV Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia;
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U62900
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DNFDFTEDEISDLLLEVENQKLFKVRLDFVKNDRMATI SGLQMLQALKSLGKIFKS IP
DSSELLADKFFEDFVIYYLISNTSEESISKKINLPDVYSHFEIKNVNLEEKKYRLKED
DEAPFKENKNIKKNSPISVNLIRIDSKKIDYILNLVSEAVISKSSYNQINSEMITLFY
NENYFYDYQESFQRNFLLDLKIVFKDAGITLEDEIESHINSLMSFKMEKALKDISELR
NSFFRLLQNKEMTSGRLSRITTDLHESVLKTYMLPISNIFSRFTRVYBDLFKKLNKI
NSFFRLLODKSWINDHCVRNSMDHGLETVEERVKRGKSKAGTIILRAKN
EGNVISTEIEDDKSVIDDLVDPLMHCVRNSMDHGLETVEERVKRGKSKAGTIILRAKN
EGNVISTEIEDDKSVIDDLVDPLMSSEGIGTIFKKLDFLTLVIOIGLLVKSGSETY
VIPLNNVLETHRITEHDIKLLENYHEVYNLRDEVISVLRLDKLFNTTRDDSLIEKFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id-"AAB96835.1"
/db_xref="piD:g1113815"
/db_xref="GI:111815"
/db_xref="GI:1DLENEEILGVFFEEAQNLVDILEENIMSLEDDPNNSDTID
EIFRAAHTLKGSSASLDMELSDFTHIVEDVFDAIRDGKVNINNDLVDLLLSSLDVIK
EMLALRIDGKVYLNDISDLKSKLKQFLVIDDQTFIKRFDGNSIKNNFCLSESDLEEIR
EGLGIGQKVLRISVVFNSNSNHEVENGGLKIFNILKNLGSVLHTPKYEQIIDDKFLK
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/transl_table=11
/protein_id="AAC44769.1"
                                                                                                                                   /strain="212"
/db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="involved in chemotaxis"
/product="histidine kinase"
                                                          /note="orfA"
                                                                                                               /clone="pW1 and pW2"
                                       'codon_start=3
                                                                            'function="unknown"
                                                                                                                                                                      organism="Borrelia burgdorferi"
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Pred. No. 2.2;
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RESULT
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CEY73F8_
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L.inundata chloroplast rbcL gene.
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1566. .>1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Flam protein"
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/db_xref="PID:g1575447"
/db_xref="PID:g1575447"
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/KRADFSSTRLDLTNYNDYVYSGASGIVKPEDMVVDLGINMSVYLTBSARLQFIKNSV
VAPAVKSESKRYAGDTILGVRVLFPSSYSQSSAMIMPPFKIPFYSGESGNQPLGKGLI
DNIKTMKEIKVSVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPNYIP
NISSRIIKDDVPNYPLASSKMRFKAFRVSKSHSSKVKNFIFYVKDLRVLYDKLSVSID
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473. .1498
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SNEGFSFGFLLSDSRFLYSFLKNGVYYVNLSREFYDSFNNGDYNESFDVKVNLFAMSL
IKTMRFNYPGKIKKIIILVEGCILKEQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="CheA protein"
/protein_id="AAC44771.1"
/db_xref="PID:g1575448"
/db_xref="GI:1575448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1566. .>1655
/gene="cheA"
/function="chemotaxis histidine kinase"
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                                                                                                                                                                                                                                                                                                       4 fragments
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/function="putative flagellar
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/db_xref="GI:1575446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MEILDLENEELLGVFFEEAQNLVDILEENI"
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95.0%;
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310000
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x94370.1
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S.douglasi
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Phylogeny of Lycopodiaceae (Lycopsida) and the relationships of Phyloglossum drummondil Kunze based on rbcL sequences Int. J. Plant Sci. 158, 862-871 (1997)
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Lycopodiella inundata
Chloroplast Lycopodiella inundata
Chloroplast Lycopodiella inundata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Lycopodiophyta; Lycopodiopsida; Lycopodiales; Lycopodiaceae;
                                                                                                                                                                                                                                                                                                                                         l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-SEP-1996) N. Wikstrom, Department of Botany, Stockholm University, S-10691, Stockholm, SWEDEN Location/Qualifiers
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Y07938.1 GI:2808612
                 Saccharomyces douglasii.
Saccharomyces douglasii
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                      CBP2 gene.
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Saccharomycetaceae;
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                                                                                                                                                  .douglasii CBP2
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/translation="TKTSVGFKAGVRNYRITYHTPDYETKDTDILAAFRMTPOPGVPP
/translation="TKTSVGFKAGVRNYRITYHTPDYETKDTDILAAFRMTPOPGVPP
EEAGAAVAAESSTGTWTTVMTDGTSLDRYKGGCYDIEPVAGEKDQYIAYVAYPLDLF
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RPLLGCTIKFKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPMKWRDRFLFVAEA
LYKAQAETGEIKGHYLNVTAGTYEEILKRAQCAKKLGAPIVMHDYLTGGFTANTSLAH
YCRDNGLLHHIRAMHAVIDRQKNHGTHFRVLAKALRNSGGHHHSGTVGFKLEGEDDS
ITLGFVDLLRDDYIEKDRSRGIYFTQDWVSMPGVLPVASGGIHVWHMPALTEIFGDDS
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/db_xref="PID:g2808613"
/db_xref="GI:2808613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGNEIIREASKWSAELA
                                                                                           GI:1149547
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/product="ribulose=1,5-bisphosphate carboxylase/oxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="rbcL"
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                                                                                                                                                  3022 bp
CBP2 gene.
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Saccharomyces.
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Li,G.Y., Tian,G.L., Slonimski,P.P. and Herbert,C.J.
The CBP2 gene from Saccharomyces douglasii is a functional homologue of the Saccharomyces cerevisiae gene and is essential for respiratory growth in the presence of a wild-type (intron-containing) mitochondrial genome wol. Gen. Genet. 250 (3), 316-322 (1996)
                                                                                                                                                                                                                                        92149494
U87072.1
                                                   Marchantlopsida; Calobryales; Haplomitriaceae; Haplomitrium.

1 (bases 1 to 1347)
Lewis,L.A., Mishler,B.D. and Vilgalys,R.
Phylogenetic relationships of the Liverworts (Hepaticae), a embryophyte lineage, inferred from nucleotide sequence data
                                                                                                                                                                                                                                                                                                HHU87072 1347 bp DNA PDNA Haplomitrium hookeri ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, encoding chloroplast protein, partial cds.
embryophyte lineage, inferred
chloroplast gene, rbcL
Mol. Phylogenet. Evol. (1997)
2 (bases 1 to 1347)
                                                                                                                                                        Chloroplast Haplomitrium hookeri
Eukaryota; Viridiplantae; Strepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-DEC-1995) C.J. Moleculaire du CNRS, F-91198
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96180648
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/db_xref="PID:e217090"
/db_xref="PID:g1149548"
/db_xref="GI:1149548"
/db_xref="SPTREMBL:Q08996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mvnwqtlfwvslrrogsssryrykfnmenithqvfprckoafkk
Anlsyfetchlecklyrnaslmdlokmlladinaprdhyrkivfnutureksskkriqhe
Qiapiddhplslyrnlsemdhofksesemqolievrrdyrddatigefdgigifpyf
Rgigvkkntydrllkorngevpmfvnpanakfllfergepfydakgaasr
ykhraffytevdklktriisplcnlnerkttdkanagrlleregepfydakgaasr
Aadgnaytlkollersyshkiimskqinkdricpgdilatilsdegifpyfpt
ykhraffilgnkksirdfskoinkdricpgdilatilsdegifyddasr
Aadgnaytlkollersyshkiimskqinkdricpgdilatilsdegifkerildiltk
kfilnyktkydsflodictystilvisekkmogfsifonnetslerehtillotiltk
skmirifornixkfmoddlaratlmeltgetesinatigfgeaneoslganalkklan
Ollhfeckiyabeldhoftystilvistkmidtigbefaneoslgaranlkklan
Chinfeckiyabethghmhcidkkmidkstemylyelkynddlkapppokekiydniigll
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/codon_start=1
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/db_xref="taxon:46617"
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Gif-sur-Yvette,
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Yvette, FRANCE
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                      Anderson, M., Baker, J., Baldvin, J., Barna, N., Beckerly, R., Benn, J.,
Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M.,
Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,
Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W.,
Forrest, C., Funke, R., Gage, D., Gardyna, S., Geralgery, K., Grant, G.,
Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C.,
Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P.,
Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A.,
Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C.,
Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella, Miller, I.,
Vassiliev, H., Wagner, A., Wheeler, J., Wu, Y., Wynan, D.,
Vassiliev, H., Wagner, A., Wheeler, J., Wu, Y., Wynan, D.,
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19; Conserv
Stanyc - Subramanian, A., Yes., Subramanian, A., Yes.,
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Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 17, clone hRPK.756_K_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 156811)
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/db_xref="GI:21
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GGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGNEVIREACKWSPELAAACE*
263 c 324 g 392 t 4 others
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/product="ribulose-1,5-bisphosphate carboxylase/oxygenase
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/strain="93"
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CE 3 (bases 1 to 15681)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Collymore, A., Cooke, P., FitzHugh, W., Forrest, C., Funke, R., Congage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., Mychalecky, J., Makf, R., Naylor, J., Nolla, M., Morris, W., Morrow, J., Mychalecky, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-miller, I., Ye, W.J., Zhao, J. and Zody, M.

Direct Submission

AL Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 1, 1998 this sequence version replaced gi:3668105.
All repeats were identified using RepeatWasker: Smit, A.F.A. & Green, P. (1996-1997)

http://fft.com/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/screen/s
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Direct Submission
Submitted (27-AUG-1998) Whitehead Institute/MIT Center
Submitted (27-AUG-1998) Whitehead Institute/MIT Center
Research, 320 Charles Street, Cambridge, MA 02141, USA
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8892. 8981
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complement(3467, .4076)
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/rpt_family="Charlie3"
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complement(7047. .7:
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/rpt_family="Alusc"
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complement(5371
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complement/2127
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/db_xref="taxon:9606"
/clone="htapk.756_K_l1"
/clone_lib="RPCI-11 human BAC library"
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family="LTR29"
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complement(25879. 25981)
/rpt_family"Alusx"
25982. .26087
                                                                                                                                                complement(36958. .37175)
/rpt_family="L1MA10"
complement(37176. .37484)
/rpt_family="Ally"
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complement(21829. .21848)
/rpt_family="(CAAA)n"
21928. .22223
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/rpt_family="FLAM_A"
complement(37618. .37919)
/rpt_family="LIMA10"
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complement(31935. .32642)
/rpt_family="LTR8"
complement(36273. .36584)
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complement(30350 ...
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/rpt_family="MLT1G"
26939...27037
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complement(25425. .;
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/rpt_family="L2"
complement(24353. .24376)
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21113. .21475
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18917. .19024
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complement(17579. .17813)
/rpt_family="MLT1G"
18381. .18915
                                                          complement(37920. .38210)
/rpt_family="Alusc"
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36820. .36926
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20267. .20318
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/rpt_family="Alusq"
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4. .365661
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5. .31780
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1 Similarity 90.5%;
19; Conservation
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Structural analysis of Arabidopsis thaliana chromosome 5. II.

Structural analysis of Arabidopsis thaliana chromosome 5. II.

Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned Pl clones

DNA Res. 4 (4), 291-300 (1997)
                                                                                                                                    Submitted (22-AUG-1997) to the DDBJ/EMBL/GenBank databases. YasukRazu Nakamura, Kazusa DNA Research Institute, Laboratory Gene Structure 2; 1532-3; Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequence. AB006702
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Direct Submission
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/rpt_family="Aluy"

complement(41025. .41492)

/rpt_family="LIME3A"

complement(41141. .41570)

/note="Single-stranded coverage."

complement(41529. .41697)

/rpt_family="MIR"
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/note="Single-stranded coverage."
/note="Single-stranded coverage."
complement (40433. .40722)
/rpt_family="LIME3A"
complement (40724. .40747)
/rpt_family="(CAA)n"
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,complement(38721...38744)
/rpt_family="LIMA10"
complement(38759...38931)
/rpt_family="LIMC/D"
complement(39363...39654)
/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/chromosome="5"

/clone="MP012"
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P1 clone: MPO12,
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Orthotrichum
                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-APR-1999) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator Gene Structure 2: 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural Analysis of
Unpublished (1999)
(bases 1 to 13186)
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Eukaryota; Viridiplantae;
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Fax:+81-438-52-3934)
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1 15052 c 14436 g 29825 t
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/chromosome="5"
/clone="T32G24"
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2304 c 2279 g 4
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/strain="Columbia"
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               GI:4009399
                                                   1320 bp DNA
Lyelli ribulose-bisphosphate carboxylase large subunit chloroplast gene encoding chloroplast protein, partial
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94.7%;
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1 (bases 1 to 1320)
1 (bases 1 to 1320)
Goffinet, B., Bayer, R.J. and Vitt, D.H.
Circumscription and phylogeny of the Orthotrichales (Bryopsida)
inferred from rbct sequence analyses
am. J. Bot. 85, 1324-1337 (1998)
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                                                                                 Goffinet,B., Bayer,R.J. and Vitt,D.H.
Circumscription and phylogeny of the Orthotrichales (Bryopsida)
inferred from rbcL sequence analyses
Am. J. Bot. 85, 1324-1337 (1998)
                                                                                                                                                                   Chloroplast Ulota obtusiuscula
Eukaryota; Viridiplantae; Streptophyta; Er
Bryidae; Orthotrichales; Orthotrichaceae;
1 (bases 1 to 1320)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orthotrichum lyelli.
Chloroplast Orthotrichum lyelli
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryopsida;
Bryidae; Orthotrichales; Orthotrichaceae; Orthotrichum.
Direct Submission Submitted (28-MAY-1997) Department of Botany, Duke University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goffinet, B.
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                                                   Goffinet,B.
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/product="ribulose-bisphosphate carboxylase large subunit"
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QAETGEIKGHYLNATAGTCEEMMKRADERELGMPIVMHYGGFTANTTLAHYGRD
NGLLHHIRAMHAVLDRQKNIGMHFRYLAKALRLSGGHHHAGTYVGKLEGERQYTLG
FYDLLRDDYIEKDRSRGIYFTODWYSLPGVLPVASGGHWWHMPALTEIFGDDSVLQF
GGGTIGHPWGNAPGAANRVALEACYQARNEGRDLAREGNDVIREATK"
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/strain="Goffinet 3162 (ALTA)"
/db_xref="taxon:61563"
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Pred. No. 1.2e
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.2e+02;
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e; Ulota.
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Circumscription and phylogeny of the Orthotrichales (Bryopsida)
inferred from rbcL sequence analyses
Am. J. Bot. 85, 1324-1337 (1998)
2 (bases 1 to 1320)
                                                                                                                                                                                                                                                                                                                                                                                           Ulota lutea.
Chloroplast Ulota lutea
Chloroplast Viridiplantae; Streptophyta; Embryophyta;
Bryidae; Orthotrichales; Orthotrichaceae; Ulota.
                                                                                                                                                                                                                                 Submitted (28-MAY-1997) Department of Botany, Duke University, P.O.Box 90339, Durham, NC 27708
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Ulota lutea ribulose-bisphosphate carboxylase large subunit (
gene, chloroplast gene encoding chloroplast protein, partial
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Clicumscription and phylogeny of the Orthotrichales (Bryopsida)
Inferred from rbct sequence analyses
Am. J. Bot. 85, 1324-1337 (1998)
2 (bases 1 to 1320)
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Bryodixonia perichaetialis ribulose-bisphosphate carboxylase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein.
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Chloroplast Bryodixonia perichaetialis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryopsida;
Bryidae; Orthotrichales; Orthotrichaceae; Bryodixonia.
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August 18, 1999, 17:18:42; Search time 148.09 Seconds (without alignments) 35.479 Million cell updates/sec

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Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database : N\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| V52141<br>V74373<br>X20248_07<br>X20248_08                                  | T959436<br>T95887<br>V00396<br>V24850<br>V24949<br>V20203                                                     | Q45332<br>Q99602<br>Q99602<br>T41617<br>T46159<br>T68125<br>T67564 | X05954<br>X07356<br>X30451<br>Q05366<br>Q05798<br>Q05798<br>Q30109<br>Q60293 | X13238<br>T68023<br>V52367<br>V52190<br>V52184<br>T98735<br>X14096 | Q47189<br>Q47189<br>X13213<br>X13213<br>V579038<br>V57903<br>X13474<br>X13037<br>X13037<br>X20248_02<br>V27287                                                           | 4021                                   |
| Streptococcus pneu Staphylococcus aur Continuation (8 of Continuation (9 of | Human Ahreceptor DNA for epidermal Insecticidal gene H. pylori orr fogp H. pylori secreted Probe (104) for mi | epider Ah rec bean locus. lori se                                  |                                                                              | m.o c c c o n                                                      | SHP gene. Yeast S Enterococcus faeca Sequence of human Hereditary haemoch Enterococcus faeca Enterococcus faeca Continuation (3 of Full-length utroph Arabidopsis thalia | cription tinuation (2 o tinuation (3 o |

RESULT V74423/c

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Location/Qualifiers 901. .960 /\*tag= a

Staphylococcus aureus

V74423 standard; DNA; 18613 BP.

V74423;
V74423;
16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #112.

Computer readable medium; vaccine; S. aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

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| , | 1 ctaat<br>     <br>115 CTAAT | cal                                                | 1<br>1<br>01<br>uation (2 of 1<br>uence split in<br>Fragment Name<br>X20248_01<br>X20248_02<br>X20248_03<br>X20248_04<br>X20248_04<br>X20248_05<br>X20248_05<br>X20248_05<br>X20248_06<br>X20248_06<br>X20248_07<br>X20248_08<br>X20248_09                                                                                                                                                                                                                                                   |            |
|   | ctaatttttcggagatgattc<br>     | th 100<br>  Similarity 100<br>  Similarity 100     | of 10) c<br>1t into 1<br>Name<br>0<br>1<br>1<br>2<br>2<br>2<br>3<br>3<br>4<br>4<br>4<br>4<br>5<br>5<br>6<br>6<br>7<br>7<br>7                                                                                                                                                                                                                                                                                                                                                                 |            |
|   | ctaatttttcggagatgattc 21<br>  |                                                    | RESULT 1  Continuation (2 of 10) of x20248 from base 100001  Continuation (2 of 10) of x20248 from base 100001  WP Sequence split into 10 fragments LOCUS x20248  WP Fragment Name Begin End 1 10000  WP X20248_01 100001 210000  WP X20248_03 200001 310000  WP X20248_03 300001 410000  WP X20248_03 300001 510000  WP X20248_05 500001 510000  WP X20248_06 600001 710000  WP X20248_06 600001 910000  WP X20248_08 800001 910000  WP X20248_08 800001 910000  WP X20248_08 800001 910000 |            |
|   |                               | Score 21; DB 1<br>Pred. No. 0.22;<br>0; Mismatches | E M440040000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNMENTS |
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#### RESULT 2 X20248\_02 Continuation (3 of 10) of X20248 from base 200001 (Borrella burgdorferi polynucleotid WP Sequence split into 10 fragments LOCUS X20248 Accession X20248 WP Fragment Name Begin End 1 110000 WP X20248\_00 1 10001 210000 WP X20248\_02 200001 310000 WP X20248\_03 300001 410000 WP X20248\_03 300001 510000 WP X20248\_05 500001 510000 WP X20248\_06 600001 710000 WP X20248\_07 700001 810000 WP X20248\_08 800001 910715 Query Match Best Local Similarity Matches 21; Conserva 4115 CTAATTTTTCGGAGATGATTC 4135 1 ctaatttttcggagatgattc 21 Conservative 100.0%; 0 Score 21; DB 1; Pred. No. 0.22; ; Mismatches 0 0; Length 110000; 0 Gaps 0

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1. Page 641-651; 3271pp; English.

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PO 10-APR-1997; US-90

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New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 1, Page 859-860; 2054pp; English.

This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritts, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used detection and diagnosis.

Sequence 900 BP; 308 A; 183 C; 167 G; 242 T;
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PS Claim 1; Page 1284-1294; 2084pp; English.

CC A computer readable medium has been developed which has recorded on it computer readable medium has been developed which has recorded on it computer readable medium has been developed which has recorded on it computer because sequences isolated from the Enterococcus faecalis genome. CC val938 to X13919 represent these nucleotide sequences which are primary cc nucleotide sequences, also known as contigs. The computer-based system cc can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence computer faecalis in samples. They can also be used for classing senterococcul infection in an animal and monitoring progression of disease, and for identifying agents which can be used to condulate the growth or pathogenicity of Enterococcus faecalis, or can obther related organism, in vivo or in vitro. In particular the conjugation of the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcus
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14-NOV-1997; US-046009.
06-MAY-1997; US-046609.
16-MAY-1997; US-046655.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
WPI; 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polypeptides
used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis genome contig SEQ ID NO:276. Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds Enterococcus faecalis.
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This sequence represents the yeast SNFI homologous protein gene (SHPP). The yeast SHPP gene may be obtained from Nicotinia taba and may be used to control expression of invertase for the increase of control expression of invertase for the increase of control expression of invertase control expression.
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Matches 17
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Hereditary haemochromatosis subregion from an HH affected individual. Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; Iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.

Homo sapiens.

WO9814466-Al.

09-APR-1998.
30-SEP-1997; U17658.
10-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO8906286-A.
13-JUL-1989.
16-DEC-1988;
22-DEC-1987;
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Sequence
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V57903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The inventors claim an MD probe comprising a purified hybridises to at least a part of the MD gene; pure dyspolypeptide, purified NA encoding DS and antibodies (A probes are equal to or greater than 10b of one of 12 c deposited as ATCC 58666-57677. The MD gene is human, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of human muscular dystrophy (MD) cDNA.

Dystrophin; muscular dystrophy; probe; antibody; diagnosis; prenatal; heterozygote; gene therapy; genetic screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 68pp;
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Kunkel LM, Monaco A, Hoffman
WPI; 89-220587/30.
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cc haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the CC DNA or RNA for the presence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The CF gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a ROREt gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can can used in the productant of the study be used for hypophosphatemia.

So Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T;
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Best Local Similarity
Matches 17; Conser
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       Claim 1; Page 1789-1793; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome x12938 to x13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for dispossing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the
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Tsuchihashi
WPI; 98-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis genome contig SEQ ID NO:537. Enterococcus faecalis; contig; detection; Enterococcal vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                    HUMA-) HUMAN GENOME SCI INC
Barash SC, Dillon PJ, Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
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Wolff RK;
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P Fragment Name
P X20248_00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for disgnosing Enterococcual infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis; genome contig SEQ ID Enterococcus faecalis; contig; detection; E
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06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
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04-MAY-1998; U08985
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Pred. No. 63;
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Accession X20248
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26-JUN-1997.
19-DEC-1996; G03156.
24-OCT-1996; GB-022174.
19-DEC-1995; GB-025962.
26-JUL-1996; GB-015797.
(MEDI-) MEDICAL RES COUNC
Davies KE, Tinsley JM;
WPI: 97-341687/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95153
                                                                                                                                                                                      also transformed mammalian cells, used for alleviating symptoms of muscular dystrophy Claim 6; Fig 9; 78pp; English.

A utrophin gene (T74666) codes for a 395 kDa protein (W22017) that shows strong sequence similarity to dystrophin. A utrophin minigene (see also T74665) has been constructed with comprises approx. the first 2 kb and the last 4 kb of the full-length coding sequence. The smaller size of the minigene makes it suitable for cloning into viral vectors designed for specific tissue expression in muscular dystrophy gene therapy procedures. Utrophin nucleic acids and polypeptides are also useful in screening for substances that modulate utrophin binding to actin and/or the dystrophin
 V27287 standard;
V27287;
                                                                   03-OCT-1997 (first entry)
Full-length utrophin gene.
Utrophin; minigene; Duchenne muscular dystrophy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                    P-PSDB; W22017.
Nucleic acid encoding utrophin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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X20248_07
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X20248_08
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/note= "n bases at positions 724-738 code
DKKSIMYLTSL, a region absolutely
conserved between human, mouse and rat
dystrophin sequences"
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94.1%;
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0; Mismatches
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Matches 16
                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis genome contig SEQ ID NO:301.
Enterococcus faecalis; contig; detection; Enterococca vaccine; attenuation; computer readable medium; ds. Enterococcus faecalis.
WO985055-A2.
1-NOV-1998.
1-NOV-1998.
10-NAY-1997; US-066009.
R 16-NAY-1997; US-044031.
16-NAY-1997; US-046655.
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Arabidopsis thaliana antifungal MS59 homologue cDNA.
Antifungal; fungicide; MS59; sunflower; carbohydrate oxid.
Antifungal; fungicide; MS59; sunflower; carbohydrate oxid.
glucose oxidase; transgenic plant; Phytophthora; Pythium;
crop protection; disease resistance; ds.
Arabidopsis thaliana ecotype Columbia.
Key
CDS
2. 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA sequence was isolated in a BLAST screening of expressed sequence tag (dDEST) databases using sunflower cv. zebulon antifungal protein MS59 (see W55053). It comprises Arabidopsis thaliana EST Q_ATTS4954. Claimed antifungal proteins, including MS59 and its homologues encoded by isolated ESTS (see V27264-91) from Arabidopsis and rice, have a mol.wt. of 55-65 kba (SDS-PAGE), have carbohydrate oxidase activity, show anti-Phytophthora and/or anti-Pythium activity, show anti-Phytophthora end/or reduce susceptibility to infection by fungi, or expressed in host cells for use in antifungal compositions. Plants engineered to express the antifungal proteins require reduced treatments with fungicides and have a longer shelf-life.

Sequence 346 BP; 88 A; 54 C; 88 G; 108 T;
      Claim 1; Page 1354-1363; 2084pp; English.

A computer readable medium has been developed which has recorded 982 nucleotide sequences isolated from the Enterococcus faecalis X12938 to X13919 represent these nucleotide sequences which are purcleotide sequences, also known as contigs. The computer-based sequences, also known as contigs.
                                                                                                                                                    use in vac
infection.
                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polyper
used to develop products for the detection of Enterococcus a
use in vaccines for prevention or attenuation of Enterococcus
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Custers JHHV, Lageweg W, N
Sela-Buurlage MB, Stuiver
WPI; 98-230692/20.
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19-MAR-1997; EP-200831.
04-SEP-1996; EP-202466.
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.2; Page 85; 139pp;
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d from the Enterococcus faecalis genome nucleotide sequences which are primary as contigs. The computer-based system
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                                                                                                                                                                                                                                    pri polypeptide(s) - useful for vaccines to treat or prevent H. pylori pri infection, and to detect Helicobacter Claim 23; Page 851; 1481pp; English.

CC This sequence encodes a H. pylori secreted or periplasmic protein. CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, CC useful as potential H. pylori life cycle activators or inhibitors. CC were proved to the pylori (ATCC 55679) was determined from CC overlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To complete the pylori antigens for vaccine development, the amino cand sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be cisolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.

So Sequence 1275 BP; 478 A; 226 C; 280 G; 291 T;
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15742 ATTTTTAGGAGATGATT 15726
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07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. pylori secreted or periplasmic protein ORF 07gel1504orf2. Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent
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                                                                                             Conservative
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Search completed: August 18, 1999, 17:18:51 Job time: 3283 sec

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Title:
Perfect score:
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1 ctaatttttcggagatgattc
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em_est6: *
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| 58: | 57:  | 56:        | 55:  | 04:    |
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| t26 | t25: | em_est24:* | t23: | 38.77. |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| RESULT 1 C87660 LOCUS DEFINITION ACCESSION VERSION |            | C 45     | C 43                                   | Δ.       | 44               | · w      | ი ი<br>38      | , w      | wu       | ω            | ω (          | ი ი<br>31            | N             | N N                          | N        | 25       | c<br>23  | N        | 21<br>21   | , <u>_</u> | c 18         | 16          | 15       |              |          | ۰.         | 0<br>0<br>0 |          | c 7      | -           |          | n (        |             | Result<br>No. |           |
|----------------------------------------------------|------------|----------|----------------------------------------|----------|------------------|----------|----------------|----------|----------|--------------|--------------|----------------------|---------------|------------------------------|----------|----------|----------|----------|------------|------------|--------------|-------------|----------|--------------|----------|------------|-------------|----------|----------|-------------|----------|------------|-------------|---------------|-----------|
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| 7660 Mousone J0241<br>7660 Mousone J0241<br>7660   |            |          | 72.4<br>72.4                           |          |                  |          |                | Ņ        |          | , N          | ω:           | ωω                   | ω             | ω <u>.</u>                   | •        | ω.       | ω        | ω        | ω.         | ω.         |              | າ ເກ        | 5        | л <u>(</u> л | .5       | <u>ن</u> د | א .~        | 1.7      | .7:      | <b>1</b> .7 | 7        | 7          | 4 C         | Query         | do.       |
| 58<br>se fer<br>8H09 3                             |            | 9        | 271<br>393                             | 51       | ww               | -        | $\sim$ $\circ$ | 0        | A 6      | <b>~</b> (   | σ.           | 77                   | $\rightarrow$ | us a                         | N        | 4        | ~ w      | · UT     | 4 N        | 4          | wc           | v or        | 9        | $\sim$       | 0        | 4          | oω          | w        | N        | лΝ          | ν.       | 4          | . U         | Length        |           |
| 63 ` 11 +                                          |            | 49       | 24                                     | 23       | 2 2              | 23       | 22             | 22       | 21       | 20           | 46           | 42                   | 42            | 40                           | မ<br>မ   | 32       | 26       | 25       | 2 2        | 21         | 4 6          | 47          | 4        | 4 3<br>4 4   | 39       | 28         | 2 C         | 4.8      | 41       | ω<br>0 0    | 30       | 29         | ω<br>5 φ    | DB BC         |           |
| p mRNA<br>.ized one-cell-embryo<br>mRNA sequence.  | ALIGNMENTS | AI630770 | D61428<br>H84144                       | R85219   | D61333<br>D61376 | D60137   | R56172         | T91811   | T86427   | 613          | 2253         | AI146344<br>AI148129 | 2441          | 000                          | AA400732 | 5414     | 025      | W05124   | D59834     | 032        | 7936<br>2183 | AI525474    | 4269     | 276<br>4152  | 271      |            | 2335        | 56537    | 03311    | AA229337    | 22921    | 18441      | C876        | ID            | SOMMARIES |
| EST 11-MAR-1998<br>CDNA Mus musculus CDNA          |            | 30770 tx | D61428 HUM400F07B<br>H84144 vt02g09.r1 | 219 yo41 | 333 HUM1         | 137 HUMO | 172 yg92       | 811 ye02 | 427 yd87 | 613 MUS74B10 | 22530 tf86b0 | 46344 qb<br>48129 qb | 24413 SWOVL3  | 1 006063 006<br>1367nu 97680 | 00732 zv | 54148 ES | 025 zb55 | 124 za83 | <u>ت</u> م | 032 ATTS   | 21835 48     | 25474 PT    | 42694 uc | 276 C242     | 271 C242 | 87198 mk   | 23359 ME    | 65372 ti | 33116 ow | 29337 nc    | 29217 nc | 184418 mt  | .87660 C876 | On            |           |

| ACCESSION<br>NID<br>VERSION               | ž r                                                                                                                                    |
|-------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|
| C87660<br>92919617<br>C87660.1 GI:2919617 | C87660 585 bp mRNA EST 11-MAR-1998<br>C87660 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA clone J0248H09 3', mRNA sequence. |

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi.
1 (bases 1 to 300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C36783 Yuji Kohara unpublished cDNA Caenorhabditis clone yk467e5 3', mRNA sequence.
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Unpublished (1998)
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Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                    Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
                                                                                                                                                                                                                                                                        Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H.,
Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g2372924
C36783.1 GI:2372924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone yk467e5
C36783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hd@bioa.jst.go.jp.
Location/Qualifiers
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Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
                                                                                                                                                                                                                  Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hirofumi Doi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                          Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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                                                                                                                                                                                                                                                    Apr 14, 1993 this sequence version replaced
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                                                                                                                      0559-75-6240
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"
132 c 117 g 169 t 11 others
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/clone="J0248H09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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mt34h06.rl Soares mouse
5', mRNA sequence.
AA184418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project Washd-HHMI Mouse EST Project washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Ld Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 441)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:383827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
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h quality sequence stop: 439.
Location/Qualifiers
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/clone=lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
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tissue_type=whole animal"
a 52 c 58 g 91 t
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pTTT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:623003"
                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                    /clone_lib="Soares
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Best Local (
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
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Unpublished (1997)
On Sep 12, 1996 th
                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 383. [ocation/Qualifiers]
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1 (bases 1 to 424)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA229217 424 bp
nc44b01.rl NCI_CGAP_Pr3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
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                     137
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                                              /note="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 mg of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
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                  David Krizman.
75 c
                                            directionally cloned.
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1010953"
                                                                                                                                                                                                                                                                             /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Pr3"
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Pred. No. 2.7e+02;
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clone IMAGE:1010953,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
On Sep 12, 1996 th
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National Cancer Institute, Cancer Genome Anatomy
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                                         /note="Vector: pAMP10; Site_1: Not1; Site_2: ECORI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells
histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to ECORI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                    David Krizman.
                                                                                                                                                                                                                                                                                                  /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                       /sex-"Male"
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Pred. No. 2.7e+02;
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                    131 t
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Query Match
Best Local Similarity
Matches 18; Conserv

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Score 16.2; DB 30 Pred. No. 2.7e+02;

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AA777778/c
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Best Local S
Matches 18
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clone IMAGE:448583 3',
AA777778
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                                           CTCATTTTCCTGAGATGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 450)

Hillier,L., Allen,M., Bowles,L., Dubugue,T., Geisel,G., Jost,  
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2152720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 438.
Location/Qualifiers
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
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108 c 87 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
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/map="17q21"
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/db_xref="GDB:1352840"
                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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                                                                                                              77.18;
85.78;
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fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
3', mRNA sequence.
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                                                                                                              Score 16.2; DB 38 Pred. No. 2.7e+02;
                                                                                                Mismatches
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                                                                                                                           Length 450;
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Best Local
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288 CTCATTTTCCTGAGATGATTC
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                                                                                                                                                                                                       AI565372 334 bp mRNA
t173f05.x1 NCI_CGAP_Kid11 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length: 735 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Cancer Institute, Cancer Genome Anatom
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI033116 426 bp mRNA EST 0w98h04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo clone IMAGE:1654903 3', mRNA sequence.
                                                                                                 EST
                                                                                                                                                                   mRNA sequence.
AI565372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              Homo sapiens
                                                                                                                       AI565372.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

101 c 78 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host-"DH10B (ampicillin resistant)"
/note-"Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note-"Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/with a modified polylinker; Site_1: Pac I; Ste_2: Eco RI;
This is a subtracted version of the original Soares fethed
liver spleen lNFTs library 1st strand CNNN was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1654903"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="20 week-post conception fetus"
                                                                                                                       GI:4523829
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.2; DB 41;
Pred. No. 2.7e+02;
0; Mismatches 3;
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IMAGE:2137665
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AI723359/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAATTTTTTGGAGCTAATTC 223
                                                                                                                                                                                                                                                                                                 AI723359 493 bp mRNA EST ME000106.FOR Egg stage cDNA expression library Schistosoma mansoni cDNA 5' similar to P47826 6 PROTEIN PO, mRNA sequence.
Contact: Oliveira, Guilherme
Lab. Parasitologia Cel. e Mol
                                                            Oliveira,G.C. and Baba,J.
Cataloguing Schistosoma mansoni genes with expressed sequence tags
Unpublished (1998)
On Dec 20, 1995 this sequence version replaced g1:1133305.
                                                                                                                                                       Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidila; Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: :
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On May 18, 1998 th
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                   Schistosoma mansoni.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
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                                                                                                                                        (bases 1 to 493)
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/db_xref="taxon:9606"
/clone="IMAGE:2137665"
/clone=lib="NCI_CGAP_Kidil"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.18;
85.78;
                                                         this sequence version replaced gi:1133305
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FEATURES
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Email: est@watson.wustl.edu
Insert Size: 1105
High quality sequence stops: 332
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@famage.llnl.gov) for further information.
Insert Length: 1105 Std Error: 0.00
Seq primer: M13RP1
Seq primer: M13RP1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H66575 398 bp mRNA EST 18-OCT-1995
yu16h03.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
IMAGE:234005 5', mRNA sequence.
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                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
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Insert Length: 493 Std Error: 0.00
Seq primer: M13 Reverse Universal Sequ
Location/Qualifiers
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Av. Augusto de Lima 1715 Barro Preto, Belo Horizonte, MG, CEP
                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project 
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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/dev_stage="Egg"
/note="Vector: Uni-Zap XR vector, Stratagene (pBluescript /note="Vector: Uni-Zap XR vector, Stratagene (pBluescript SK).; Site_1: EcoRI; Site_2: XhoI; mRNA was extracted from eggs and the library was constructed and excised according to the manufacturer's instructions."

a 109 c 111 g 133 t
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/clone_lib="Egg stage cDNA expression library
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85.78;
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Pred. No. 2.6e+02;
0; Mismatches 3;
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1 (bases 1 to 543)

1 (bases 1, to 543)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., T., Le, M., Martin, J., Morre, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA087198 543 bp mRNA
mk22f03.rl Soares mouse p3NMF19.5 Mus
IMAGE:493661 5', mRNA sequence.
AA087198
                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
On Sep 12, 1996 this sequence version
                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                 vector to vector length is 609
Seq primer: -28M13 rev2 from Ar
                                                                                                                                    Putative full length read
                                                                                                                                                     MGI:297109
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/db_xref="GDB:3787182"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:234005"
                  /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                 Location/Qualifiers
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   /clone="IMAGE:493661"
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100.0%; Pr
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3.3e+02;
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Local Similarity 89.5%;
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C24271
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C24271
                                                                                                                                                                                                                                                                                                                              National Institute of Fruit Tree Science, Okitsu Okitsu, Shimizu, Shizuoka 424-02, Japan Tel: +81-543-69-2111
Fax: +81-543-69-2115
Email: om9330@okt.affrc.go.jp
PROJECT = Citrus Genome Analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 306)

Hisada, S., Akihama, T., Endo, T., Moriguchi, T. and Omura, M.

Expressed sequence tags of Citrus fruit during rapid cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development phase
J. Amer. Soc. Hort. Sci. 122,
On Jan 14, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mitsuo Omura
Department of Citriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Citrus unshiu.
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/strain-"Miyagawa-wase satsuma mandarin"
/db_xref-"taxon:55188"
/map-"15"
                                                                                            /tissue_type="juice sac and pulp segment"
/dev_stage="rapid developing stage"
93 c 84 g 59 t
                                                                                                                                                         (M.Omura)"
                                                                                                                                                                     /clone_lib="Miyagawa-wase satsuma mandarin orange
                                                                                                                                                                                         clone="pcMFRI804.93"
                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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75.2%;
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sequence version replaced gi:1797773
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Score 15.8;
Pred. No. 4
8; DB 39;
4.2e+02;
                  Length 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Citriculture
National Institute of Fruit Tree Science,
Okitsu, Shimizu, Shizuoka 424-02, Japan
Tel: +81-543-69-2111
Eax: +81-543-69-2115
Email: om9330@okt.affrc.go.jp
PROJECT - Citrus Genome Analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92104073
C24276.1
EST.
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C24276
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 305)
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C24276
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J. Amer. Soc. Hort. Sci. 122, 808-812 (1997)
On Jan 14, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                 g3280718
AI041524.1
                                                                                                                                                  AIO41524 305 bp mRNA
ov82a09.x1 Soares_testis_NHT
3', mRNA sequence.
AIO41524
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                                                                                 numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Citrus unshiu"
/strain="Miyagawa-wase satsuma mandarin"
/db_xref="taxon:55188"
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/clone_lib="Miyagawa-wase satsuma mandarin or
/fclone_type="juice sac and pulp segment"
/dev_stage="rapid developing stage"
3 a 94 c 86 g 59 t
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                                                                                                                  GI:3280718
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4.2e+02;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bent
                                                                                          Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                              Eukaryota; Metazoa;
Eutheria; Rodentia;
1 (bases 1 to 360)
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                          Unpublished (1996)
On Jan 19, 1998 this sequence version
                                                            Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                 Mus musculus
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AI042694.1
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/polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDl
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1643800"
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89.5%;
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Pred. No. 4.2e+02;
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                           replaced g1:2153086
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:915660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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//dev_stage="adult"

//dev_stag
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/clone_lib="Sugano mouse liver mlia"
/sex="female"
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/strain="C57BL"
/db_xref="taxon:10090"
/map="17q21"
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
FLAGELLAR FILAMENT OUTER LAYER PROTEIN (FLAA).
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MEDLINE; 98055943. S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,

FRASER C.M., CASCINS S., HUANG W.M., DODSON R., HICKEY E.K., GWINN M.,

LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,

DOUGHERTY B., TOMB J.-F., FLEISCHHANN R.D., RICHARDSON D.,

PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,

PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,

VAN VUGT R., PALMER N., ADAMS M.D., GOCRAYNE J.D., WEIDMAN C.,

VAN VUGT R., PALMER N., ADAMS M.D., HORST K., ROBERTS K., HATCH B.,

GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

SMITH H.O., VENTER J.C.;
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Bacteria; Spirochaetales; Spirochaetaceae; Borr
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PORCELLA S.F., RADOLF J.D., NORGARD M.V.;

PORCELLA S.F., RADOLF J.D., NORGARD M.V.;

Submitted (APR-1997) to the EMBL/GenBank/DDBJ

EMBL; U97363; AAB63367.1;

EMBL; U97363; AAB63367.1;

SEQUENCE 243 AA; 27299 MW; 7CB7C276 CRC32:
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substance identification. This file contains CAS Registry Numbers for easy and accurate

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## Searched by Barb O'Bryen, STIC 308-4740

## as a diagnostic reagent for Lyme disease

Flak, and the use of recombinant P37

Identification of P37 antigen as

131:83993

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trom a Lyme disease patient who had developed a prominent humoral response
   cloned from a B. burgdorferi genomic library by screening with antibody
              antibody response in Lyme disease patients. The P37 gene was
    burgdorferi is an antigen that elicits an early immunoglobulin M (IgM)
                                       The 37-kDa protein (P37) of Borrelia
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                         Journal code: HSH. ISSN: 0095-1137.
100RMAL OF CLINICAL MICROBIOLOGY, (1999 Mar) 37 (3) 548-52.
                                                                          SOURCE:
                                                rbg9@cdc.gov
   Health and Human Services, Fort Collins, Colorado, USA..
  and Prevention, Public Health Service, U.S. Department of
Center for Infectious Diseases, Centers for Disease Control
     Division of Vector-Borne Infectious Diseases, National
                                                               CORPORATE SOURCE:
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     Gilmore R D Jr; Murphree R L; James A M; Sullivan S A;
                                                                          : AOHTUA
                early lyme disease is the flak gene product.
             immunoblot band (P37) used in serodiagnosis of
                     The Borrelia burgdorferi 37-kilodalton
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                  produced as a fusion protein with the T7 gene 10 product.
                          embodiment, the recombinant P37 (Flah) antigen is
          any antibody specifically bound to said protein. In a preferred
                    said sample with recombinant P37 (Flak), and detecting
  infection comprising obtaining a serum sample from a patient, contacting
                The invention provides an assay for detecting Lyme disease
           improved serol. tests for exposure to Lyme disease spirochetes.
      to B. burgdorferi infection and is significantly suitable for use in
         Flat) is a prominent antigen in the early humoral immune response
                  burgdorferi. The invention also demonstrates that P37 (
                           protein of the periplasmic flagella of Borrelia
                                       sufiden P37 as Flat, an outer sheath
  infection. The invention describes the definitive identification of the
              rime qraesse' barficularly in persons with recently acquired
 The invention provides reagents and improved methods for serodiagnosis of
                                                          PRIORITY APPLM. INFO.:
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                                 PCT Int. Appl., 34 pp.
                                                                          SONKCE:
                                 Biomerieux, Inc., USA
                                                             PATENT ASSIGNEE (S):
       Gilmore, Robert D., Jr.; Johnson, Barbara J. B.
                                                                     INVENTOR(S):
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the standardization of the present generation of IgM serologic tests. protein can be utilized as a marker in diagnostic immunoblots, aiding in set of defined antigens for the serodiagnosis of early Lyme disease. This the recombinant. Recombinant P37 may be a useful component of a negative for the B. burgdorferi P37 protein did not react with anti-P37 reactivity. Lyme disease patient samples serologically with early Lyme disease that had been scored positive for B. burgdorferi IgM immunoblots using serum samples from patients clinically diagnosed -kDa E. coli protein. The recombinant antigen was reactive in gene construct with the leader peptide deleted and fused to a 38 P37 expression was accomplished in Escherichia coli by using a sheath protein of the periplasmic flagella. Recombinant the identity of P37 to be Flah, an outer to the P37 antigen. DNA sequence analysis of this clone revealed

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correlates with severe and prolonged Lyme arthritis and the The immunoglobulin (IgG) antibody response to OspA and OspB 68LT8066

arthritis. IgG response to P35 correlates with mild and brief

School of Medicine, New England Medical Center, Tupper Division of Rheumatology/Immunology, Tufts University Akin E; McHugh G L; Flavell R A; Fikrig E; Steere A C

(ZMAIN) 8EZOS-AA Research Institute, Boston, Massachusetts O2111, USA.

INFECTION AND IMMUNITY, (1999 Jan) 67 (1) 173-81.

Journal code: GO7. ISSN: 0019-9567.

Journal; Article; (JOURNAL ARTICLE) United States

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burgdorferi proteins that may have a role in chronic Lyme arthritis, we In an effort to implicate immune responses to specific Borrelia

whereas during maximal arthritis, the higher the IgG response to OspA and earlier in the infection, the milder and briefer the subsequent arthritis, duration of arthritis. Thus, the higher the IgG antibody response to P35 to a C-terminal epitope of OspA, correlated directly with the severity and maximal arthritis, the levels of IgG antibody to OspA and OspB, especially severity or duration of maximal arthritis. In contrast, during periods of the levels of 1gG antibody to P35 correlated inversely with the subsequent responses to OspA and OspB. During early infection and early arthritis, developed weeks later; and months to years later, 64% of patients had P37, and P41; reactivity with OspE, OspF, P39, and P93 often earliest responses were usually to outer surface protein C (OspC), P35, correlated with the severity and duration of maximal arthritis. The during early infection, early arthritis, and maximal arthritis, were antibody responses to 10 recombinant B. burgdorferi proteins, determined Lyme disease. In these patients, the immunoglobulin G (IgM) and IgG serial serum samples from 25 patients monitored throughout the course of studied the natural history of the antibody response to B. burgdorferi in

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flagellar protein of Borrelia burgdorferi. Structure and expression of the Flak periplasmic : HILLE:

Department of Microbiology and Immunology, Robert C. Byrd CORPORATE SOURCE: Ge Y; Li C; Corum L; Slaughter C A; Charon N W : AOHTUA

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DUPLICATE 4
                                 Tel Answer 5 of 25 caba copyright 1999 cabi
                                    flagellin proteins of other bacteria.
  the PFs of B. burgdorferi and that they are regulated differently from
          together, the results indicate that both Flam and Flam comprise
   was antigenically well conserved in several spirochete species. Taken
                   Treponema pallidum anti-Flam serum indicated that Flam
        regulated on the translational level. Western blot analysis using
                ofher spirochete flagellar proteins, Flah is likely to be
    These results suggest that, in agreement with data found for FlaB and
             the wild-type amounts, it failed to synthesize Flak protein.
         this mutant still synthesized flam message in amounts similar to
 spontaneously occurring PF mutant of B. burgdorferi (HB19Fla-). Although
              hyodysenteriae. We also tested if Flah was synthesized in a
      glycosylation, and thus it resembles its counterpart from Serpulina
               Flah, we found that it was posttranslationally modified by
         Flam was expressed at a lower level than Flab. In characterizing
                   to find Flak. Unlike other spirochetes, B. burgdorferi
 purify B. burgdorferi PFs, and our results explain in part their failure
            Flak in the isolated PFs. Sarkosyl has been used by others to
       the other hand, purifying the PFs by using Sarkosyl resulted in no
 purified with the PFs in association with the 41.0-kDa FlaB protein. On
                             PFs, we found that the 38.0-kDa Flah protein
  detail. Using Triton X-100 to remove the outer membrane and isolate the
          results led us to analyze the PFs and {\tt Flak} of B. burgdorferi in
expressed in B. burgdorferi and that it mapped in a fla/che operon. These
                  core of Flab. We recently found that a flah homolog was
         spirochete species are comprised of an outer layer of Flah and a
       only one flagellin protein (FlaB). In contrast, the PFs from other
burgdorferi flagellar filaments indicate that these organelles consist of
       and overlap in the center of the cell. Most descriptions of the B.
  flagella (PFs). The PFs are subterminally attached to the cell cylinder
     sheath, and within this sheath are the cell cylinder and periplasmic
     features common to other spirochete species. Outermost is a membrane
 The spirochete which causes Lyme disease, Borrelia burgdorferi, has many
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                       Journal; Article; (JOURNAL ARTICLE)
                                             United States
                                                                  PUB. COUNTRY:
                       Journal code: HH3. ISSN: 0021-9193.
      100RNAL OF BACTERIOLOGY, (1998 May) 180 (9) 2418-25.
                                                                        SOURCE:
                                            (GIAIN) EPYESIA
                                                              CONTRACT NUMBER:
                               Morgantown 26506-9177, USA.
         Health Sciences Center, West Virginia University,
                                  Minnifield
                      9664395
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Cloning and expression of the 44-kilodalton major TITLE: 948909086 DOCUMENT NUMBER: 1998:163535 CABA ACCESSION NUMBER:

granulocytic ehrlichiosis agent and application of outer membrane protein gene of the human

the recombinant protein to serodiagnosis

Wormser, G. P.; Hechemy, K. Zhi, W.; Ohashi, W.; Rikihisa, Y.; Horowitz, H. W.;

Veterinary Medicine, The Ohio State University, Department of Veterinary Biosciences, College of

Columbus, OH, USA.

Journal of Clinical Microbiology, (1998) vol. 36,

No. 6, pp. 1666-1673. 31 ref.

LETT-S600 :NSSI

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**SONKCE:** 

: AOHTUA

CORPORATE SOURCE:

English

A 44-kDa major outer membrane protein of the human granulocytic ЯΑ

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purified HGE agents. simpler serodiagnosis for HGE than the use of whole infected cells or rP44 protein as antigen would provide a more specific, consistent, and recombinant antigen per dot was used. The use of the affinity-purified densities of the dot reactions and the IFA titres when >50 ng of immunoblot assay. There was a positive correlation between the colour ranging from 1:20 to 1:2560 gave distinct positive reactions in a dot Sera from 20 HGE patients with indirect fluorescent-antibody (IFA) titres agent and B. burgdorferi reacted positively with rP44 and the HGE agent. serum reacted with rP44. Sera from 2 patients coinfected with the HGE chaffeensis serum nor rabbit anti-Borrelia burgdorferi that rP44 is an HGE-E. equi group-specific antigen. Weither human anti-E. horse anti-Ehrlichia equi serum recognized the rP44 protein. This suggests (from patients in New York State, USA), a horse anti-HGE serum, and a 38 kDa were recognized. 11 HGE patient serum samples agent strains tested except strain 2, in which 3 proteins of 42, 40, and anti-rP44 serum reacted with 44- to 42-kDa proteins in 6 different HGE dot blot immunoassay. Western immunoblot analysis showed that mouse affinity-purified rP44 was evaluated by Western immunoblot analysis and expressed by using expression vector pET30a. The reactivity of the the genome of the HGE agent. The recombinant 44-kDa protein (rP44) was results revealed the existence of multigenes homologous to the P44 gene in A gene encoding this protein was cloned and sequenced. Southern blot ehrlichiosis (HGE) agent is an immunodominant antigen in human infection.

ACCESSION NUMBER: WEDTINE 1999023007 Tel Pusmer 6 of 25 medrine DUPLICATE 5

Differential expression of Borrelia burgdorferi genes

during erythema migrans and Lyme arthritis. TITLE:

Fikrig E; Feng W; Aversa J; Schoen R T; Flavell R A

Department of Internal Medicine, Yale University School of CORPORATE SOURCE: : AOHTUA

Medicine, New Haven, Connecticut 06520-8031, USA.

JOURNAL OF INFECTIOUS DISEASES, (1998 Oct) 178 (4) **SOURCE:** 

.102-86II

Journal code: IH3. ISSN: 0022-1899.

United States FUB. COUNTRY:

99023007

Journal; Article; (JOURNAL ARTICLE)

English **IPANGUAGE:** 

ENTRY MONTH: T0666T Abridged Index Medicus Journals; Priority Journals LIFE SECWENT:

Borrelia burgdorferi, the agent of Lyme disease, selectively expresses ЯA ₱0106661 ENLKA MEEK:

ruduced in human infection; these results are the first direct These data show that ospA is repressed while p35 and  ${f p37}$  are with Lyme arthritis. ospA mRNA was not identified in any of these tissues. migrans biopsy specimens from 2 patients and in the synovium of 1 patient protective immunity. p35 and p37 mRNA were detected in erythema induced by spirochetes during murine Lyme borreliosis and play roles in trials. p35 and p37 were also assessed because these genes are ticks during engorgement and is a vaccine candidate in phase III clinical ospA was investigated because OspA is down-regulated by B. burgdorferi in using RNA-polymerase chain reaction, from 3 patients with Lyme disease. gene expression during human infection was examined in tissue specimens, denes in the arthropod vector and mammalian host. Specific B. burgdorferi

disease. demonstration of differential B. burgdorferi gene expression during Lyme

1999:50456 CAPLUS ACCESSION NUMBER: CAPLUS COPYRIGHT 1999 ACS FINIMER 7 OF 25

130:04463 DOCUMENT NUMBER:

DOCUMENT NUMBER:

P37 proteins, expressed in vivo, elicit Borrelia burgdorferi P35 and TITLE:

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detected in humans infected with B. burgdorferi. S.c. injection of mice
               proteins were prepd. A humoral response to P35 and P37 was
           P37 proteins were mapped to sep. plasmids. Antibodies to these
        genes were isolated and sequenced. The genes for the P21, P35 and
antisera from mice infected with live B. burgdorferi spirochetes. Several
    with antisera from mice inoculated with killed B. burgdorferi and with
were identified by differential screening of a B. burgdorferi DNA library
infection of mice but not expressed by in vitro cultures of B. burgdorferi
 selectively expressed in vivo is also disclosed. Genes expressed during
antibodies are claimed. A method for identifying bacterial genes that are
      antibodies to these proteins, and diagnostic use of the proteins and
       identified. Vaccines comprising the novel B. burgdorferi proteins,
      cultures of B. burgdorferi, as well as genes for these proteins, are
are produced during infection of a host but are not expressed by in vitro
          Lyme disease are disclosed. Novel B. burgdorferi proteins which
        Methods and compns. for the prevention, treatment and diagnosis of
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                                PCT Int. Appl., 115 pp.
                                                                          SONKCE:
             Barthold, Stephen W.; Flavell, Richard A.
    Xale University, USA; Fikrig, Erol; Suk, Kyoungho;
                                                             PATENT ASSIGNEE(S):
                                    Flavell, Richard A.
    Erkrid, Erol; Suk, Kyoungho; Barthold, Stephen W.;
                                                                     INVENTOR(S):
                                        of Lyme disease
 compositions for prevention, treatment, and diagnosis
            expressed during infection and methods and
                         Borrelia burgdorferi proteins
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                                              128:31107
                                    1997:746160 CAPLUS
                                                               ACCESSION NUMBER:
                                 TEI FURMER 8 OF 25 CAPLUS COPYRIGHT 1999 ACS
                                               B31 open reading frame BBK32.
         burgdorferi. Nature 390, 580-586) is designated as B. burgdorferi
                                    of a Lyme disease spirochaete, Borrelia
 complete gene sequence (see Fraser C. M., et al. [1997]. Genomic sequence
    sedneuce. The remaining 813 nucleotides of the gene are correct. The
        uncjeotides of the p35 sequence are part of the pBluescript vector
                              Borrelia burgdorferi sequence. The first 114
   The initial portion of the p35 sequence reported in this paper is not a
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                  Sch. Med., New Haven, CT, 06520, USA Immunity (1998), 9(5), No pp. Given
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  Wen; Telford, Sam R., III; Flavell, Richard A. Section Rheumatology, Dep. Internal Med., Yale Univ.
                                                               CORPORATE SOURCE:
   Eikrig, Erol; Barthold, Stephen W.; Sun, Wei; Feng,
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    protective immunity. [Erratum to document cited in
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INFECTION AND IMMUNITY, (1997 Jul) 65 (7) 2992-5. (GIAIN) EPYESIA University, Morgantown 26506-9177, USA. Départment of Microbiology and Immunology, West Virg∱ associated with Lyme disease. sheath protein, is not an immunodominant antigen Flah, a putative flagellar outer 97342782 WEDTINE 97342782 ACCESSION NUMBER: Medwill Tel Answer 9 of 15 WEDFINE DUPLICATE burgdorferi, but P21 did not protect mice from tick-mediated with P35 and  $\stackrel{(x_2)}{1}$  may protect mice from challenge with B. 966400/60 Minnifield

Flak was recently found to be associated with flagellar

filaments of Borrelia burgdorferi. We tested whether antibodies to this

Escherichia coli, truncated proteins which lacked the N-terminal signal Although overproduction of intact Flam was highly toxic to

sera from two patients reacted with both recombinant and native Flak is not an immunodominant antigen in Lyme disease. However, from mammalian hosts infected with B. burgdorferi indicated that sequence could be successfully overexpressed. Immunoblotting with sera

Flat protein, suggesting that B. burgdorferi Flat was

WEDFINE 900ZTEL6 ACCESSION NUMBER:

Ge Y; Old I G; Girons I S; Charon N W : AOTTUA

Department of Microbiology, West Virginia University, CORPORATE SOURCE:

Journal code: BXW. ISSN: 1350-0872.

JOURNAL ARTICLE; (JOURNAL ARTICLE)

Priority Journals

English

60L66T

ENGIAND: United Kingdom

FUB. COUNTRY:

MICROBIOLOGY, (1997 May) 143 ( Pt 5) 1681-90. SOURCE:

(GIAIN) EPTSIA

CONTRACT NUMBER:

Morgantown 26506-9177, USA.

GENBYNK-NG2901; GENBYNK-NG6699

initiated by a sigma 70-like promoter.

The flgk motility operon of Borrelia burgdorferi is TITLE:

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Tel Answer 10 of 25 Medrine

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LANGUAGE:

proteins in other spirochetal infections show an increase in titer.

protein are a good indicator of infection, as antibodies to Flah

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Priority Journals; Cancer Journals LIFE SECWENT: English : ADAUDNAL

Journal; Article; (JOURNAL ARTICLE)

United States FUB. COUNTRY: Journal code: GO7. ISSN: 0019-9567.

**SOURCE:** 

CONTRACT NUMBER:

CORPORATE SOURCE:

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TITLE: DOCUMENT NUMBER:

Searched by Barb O'Bryen, STIC 308-4740

into a promoter probe cat vector revealed that the flyk promoter element 70-1ike promoter upstream of flbF. Subcloning the flgK promoter element revealed that transcription of the flgk operon is initiated by a sigma to orfX are transcribed as a single mRNA, and primer extension analysis assembly. Reverse transcriptase-PCR analysis indicated that flbF through filament to the hook and are required for the last stage of flagellar bacteria, the hook-associated proteins HAP1 and HAP3 connect the flagellar orfX (function unknown), and maps at 185 kb on the chromosome. In other of flbF (function unknown), flgk (encoding HAP1), flgL (encoding HAP3) and which is initiated by a sigma 70-like promoter. The flgK operon consists sequenced. This cluster comprises an operon, designated the flgk operon, A cluster of flagellar genes of Borrelia burgdorferi was identified and

| e e e            | San Mills | Mi i i     | ** 6           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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flagellar genes is evidently different from that of other bacteria. in the later stage of flagellar assembly, the regulation of B. burgdorferi 70-like promoter rather than a unique flagellar sigma factor is involved promoter element into the promoter probe cat vector. Because a sigma promoter element, no activity was detected after subcloning a flab the putative sigma gp3-34-like promoter for flab. In contrast to the flgk consistent with the presence of a sigma 70-like promoter in addition to downstream of the reported start site. The sequence around -10 and -35 are transcription of this gene. A transcriptional start point was found 1 bp sigma gp33-34-like promoter has been reported to be involved in the flab) was re-examined. flab encodes the flagellar filament protein, and a bromoter element of the flagellin gene (fla, hereafter referred to as the flgk promoter was still functional. Based on these results, the typhimurium which lacked a functional flagellar-specific sigma 28 factor, In addition, when this construct was transformed into a flih mutant of S. had strong activity in both Escherichia coli and Salmonella typhimurium.

SDSDDTL6 DOCUMENT NUMBER: **YCCEZZION NUMBEK:** WEDTINE SPSPPI76 DUPLICATE 7 Tel Fire II of 25 medrine

An unexpected flah homolog is present and

expressed in Borrelia burgdorferi.

Ge Y; Charon N W

Department of Microbiology and Immunology, West Virginia CORPORATE SOURCE:

University, Morgantown 26506-9177, USA.

DE01S040 (NIDK) (GIAIN) EPTESIA CONTRACT NUMBER:

JOURNAL OF BACTERIOLOGY, (1997 Jan) 179 (2) 552-6. **SOURCE:** 

Journal code: HH3. ISSN: 0021-9193.

United States PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE)

English

OTHER SOURCE: GENBYNK-062900 LIFE SECWENT: Priority Journals LANGUAGE:

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TITLE:

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onter speath of Flak proteins and a core of most other spirochete species are complex: these PFs contain an Borrelia burgdorferi are composed of only one flagellin protein. The PFs Most investigators have assumed that the periplasmic flagella (PFs) of

terminus. Based on reverse transcription-PCR and primer extension B. burgdorferi Flah has a conserved signal sequence at its N Flak from other spirochetes. Like other Flak proteins, homolog with a deduced polypeptide having 54 to 58% similarity to of B. burgdorferi 212, we were surprised to find a flam gene filament of Flab proteins. During an analysis of a chemotaxis gene cluster

from Treponema pallidum and a lysate of B. burgdorferi showed strong a motility-chemotaxis operon. Immunoblots using anti-Flah serum analysis, this flam homolog and five chemotaxis genes constitute

reactivity to a protein of 38.0 kDa, which is

consistent with the expression of flat in growing cells.

**YCCEZZION NOWBEK:** WEDTINE \$688TEL6 DUPLICATE 8 rel former is of 25 medrine

Borrelia burgdorferi P35 and P37 proteins, TITLE: DOCUMENT NUMBER: \$688TEL6

expressed in vivo, elicit protective immunity [published

erratum appears in Immunity 1998 Nov;9(5):following 755].

Eikrid E; Barthold S W; Sun W; Feng W; Telford S R 3rd; : AOHTUA

Flavell R A

Department of Internal Medicine, Yale University School of CORPORATE SOURCE:

Medicine, New Haven, Connecticut 06520, USA.

(**GIAIN**) **ZI832-IA** CONTRACT NUMBER:

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FUB. COUNTRY: Journal code: CCF. ISSN: 1074-7613.

United States

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English

Priority Journals LIFE SECWENT:

p35 and p37 are Borrelia burgdorferi genes encoding 35 and ЯA 8076e1 ENTRY MONTH:

37 kDa proteins. The gene products were identified by

selectively expressed in vivo. ELISA, using P35 and P37, showed Northern blot and RT-PCR analyses confirmed that these genes were from B. burgdorferi infected- and B. burgdorferi-hyperimmunized mice. differential screening of a B. burgdorferi expression library with sera

borreliosis developed P35 or P37 antibodies. Mice developed peak that infected mice (5 of 5, 100%) and patients (31 of 43, 72%) with Lyme

challenge with 10(2) B. burgdorferi, and P35 and P37 antisera Mice given both P35 and P37 antisera were protected from IgG titers to P35 and P37 within 30 days, followed by decline.

challenge. The use of in vivo-expressed antigens such as P35 and also afforded protection when administered 24 hr after spirochete

tor understanding the role of B. burgdorferi-specific immune responses in P37 represents a new approach for Lyme disease serodiagnosis and

ACCESSION NUMBER: WEDFINE P1871P79 rel busmer 13 of 25 medrine DUPLICATE 9

Molecular characterization of a flagellar/chemotaxis operon **PI811P16** 

in the spirochete Borrelia burgdorferi.

Ge X; Charon N W

Department of Microbiology and Immunology, West Virginia

University, Robert C. Byrd Health Sciences Center,

(GIAIN) EPTESIA Morgantown 26506-9177, USA.

EEWS WICKOBIOFOGX FETTERS, (1997 Aug 15) 153 (2) 425-31.

lournal code: FML. ISSN: 0378-1097.

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A chemotaxis gene cluster from Borrelia burgdorferi, the spirochete that ΆA ENTRY MONTH: TIL66T

bacteria. chemotaxis apparatus of B. burgdorferi compared to those of other results taken together suggest both similarities and differences in the consistent with two cheA homologs being present in this organism. The two reactive proteins in the cell lysates of B. burgdorferi that is Western blot analysis using antibody to Escherichia coli CheA resulted in genes and the upstream flagellar gene flam constitute an operon. Gram-positive bacteria. RT-PCR analysis indicated that the chemotaxis branch with Treponema pallidum and is closely associated with Archea and analysis of CheY indicated that B. burgdorferi constitutes a distinct significantly different from the homolog of other bacteria. Phylogenetic for B. burgdorferi CheW and CheY were well conserved, the size of cheW was reading frame we identified as cheX. Although the major functional domains contained three chemotaxis gene homologs (cheA, cheW and cheY) and an open causes Lyme disease, was cloned, sequenced, and analyzed. This cluster

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.э .я Trueba, G. A.; Old, I. G.; Saint Girons, I.; Johnson, : (2) AOHTUA

CORPORATE SOURCE:

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Searched by Barb O'Bryen, STIC 308-4740

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APPLICATION NO.

U.S., 112 pp. Cont.-in-part of U.S. Ser. No. 780,261,

on their surface and use of recombinant mycobacteria Recombinant mycobacteria expressing Borrelia antigen

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the surface of the mycobacteria. Mycobacteria which may be transformed protein or fragment by enabling the protein or fragment to be expressed on fragment. Such expression vectors increase the immunogenicity of the protein comprising a lipoprotein or lipoprotein segment and the protein or

protein or fragment is described. The mycobacteria express a fusion thereof, which is heterologous to the mycobacteria which express the lipoprotein, and a second DNA sequence encoding a protein, or fragment comprises a first DNA sequence encoding at least a secretion signal of a Yu expression vector for expressing a protein in mycobacteria, which

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CODEN: NSXXFW abandoned.

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Medimmune, Inc., USA

ss vaccines for Lyme disease

toward elucidation of a possible role of chemotaxis in virulence of the B. afZelii, resp. Identification of cheA and cheW is the first step on the linear chromosomes of B. burgdorferi sensu stricto, B. garinii and cheA and cheW form an operon with an upstream, unidentified ORF. The cheA and cheW homologs were located at 722-737 kbp, 738-768 kbp and 743-824 kpb

bacterial CheW. Using reverse transcription PCR, we demonstrated that 195-amino-acid protein which displayed a high level of similarity to immediately downstream from the putative borrelial cheA gene encoded a

location of the histidine autophosphorylation domain very close to the N particular, hallmarks of a histidine kinase family were found such as the identical residues) to the CheA of several genera of eubacteria. In encoding an 864-amino-acid protein with significant similarity (53-64.6% obtained from the CT strain identified a 2,592-bp open reading frame (ORF)

gene walking PCR and construction of a .lambda. library were used to identify the putative cheA gene. Sequence anal. of the DNA fragments

as polymerase chain reaction (PCR) using degenerate primers, random-primed and cheW were cloned and characterized. A combination of strategies such

terminus and the nucleotide-binding site. A second ORF located

Stover, Charles K.

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Medical school, Minneapolis, MW, 55455, USA Res. Microbiol. (1997), 148(3), 191-200

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BCG. Mice vaccinated with these recombinant BCG were protected from antigen gene were prepd. The OspA antigen was presented on the surface of kDa antigen promoter and signal sequence fused to B. burgdorferi OspA Recombinant BCG expressing a chimeric gene comprising M. tuberculosis 19 purgdorferi, the causative agent of Lyme disease. wherein the mycobacteria express a surface protein of Borrelia formation of live bacterial vaccines against **Lyme** disease expression vectors of the present invention may be employed in the with the expression vector include mycobacteria such as BCG. The

WEDFINE 96110942 Tel Answer 16 of 25 Medrine DUPLICATE 10

TITLE:

Borrelia burgdorferi and Borrelia hermsii.

INFECTION AND IMMUNITY, (1996 Jan) 64 (1) 262-8.

Anda P; Gebbia J A; Backenson P B; Coleman J L; Benach J L

Centro Nacional de Microbiologia, Virologia e Immunologia

Sanitarias, Instituto de Salud Carlos III, Madrid, Spain.

A glyceraldehyde-3-phosphate dehydrogenase homolog in

24601196

DOCUMENT NUMBER:

S0966T

English

United States

(RMAIN) 22404-AA (diain) Paors-ia

**YCCESSION NUMBER:** 

challenge with B. burgdorferi.

Expression and sequence analysis of a Treponema pallidum DOCUMENT NUMBER: LT8L9T96

: AOHTUA

**YCCESSION NUMBER:** 

ENTRY MONTH: OTHER SOURCE:

LIFE SECWENT:

FUB. COUNTRY:

CONTRACT NUMBER:

CORPORATE SOURCE:

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to T. pallidum and Borrelia burgdorferi proteins. dene, tpn38(b), encoding an exported protein with homology

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glycolytic pathway. GAPDH may play a similar role in borrelias. other functions in addition to its traditional enzymatic role in the the chromosome of each borrella. In other bacterial species, GAPDH has pybridization studies indicated that the gene encoding GAPDH is located on

> stearothermophilus were 59.2% and 58.8% respectively. Southern identities of B. burgdorferi and B. hermsii with Bacillus

prokaryotes successfully amplified this gene homolog in both B. brimers constructed from highly conserved regions of gapdh of other subsurface localization for the Borrelia GAPDH activity. Degenerate but not in live, intact organisms, indicating the possibility of a

the Lyme disease agent, and Borrelia hermsii, an agent of American

A polyreactive monoclonal antibody recognized a 38.5-kDa

GENBANK-U28760; GENBANK-U28761

Priority Journals; Cancer Journals

Journal; Article; (JOURNAL ARTICLE)

Journal code: GO7. ISSN: 0019-9567.

Stamm L V; Hardham J M; Frye J G

between B. burgdorferi and B. hermsii at the amino acid level. Amino acid analysis of the 838-bp probes for each borrelia indicated 93.9% identity burgdorferi and B. hermsii. Nuclei acid and deduced amino acid sequence

pathogenic spirochetes and other prokaryotes and eukaryotes as well. GAPDH activity was detected in sonicates of both B. burgdorferi and B. hermsii relapsing fever. This monoclonal antibody also recognized GAPDH from other

dlyceraldehyde-3-phosphate dehydrogenase (GAPDH) in Borrelia burgdorferi, polypeptide with amino-terminal sequence identity to conserved regions of

Department of Epidemiology, School of Public Health, CORPORATE SOURCE:

University of Worth Carolina, Chapel Hill 27599-7400, USA..

lstamm@email.unc.edu

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EEWS WICKOBIOTOGX TELLERS' (1880 191 132 (1) 21-63: **SOURCE:** 

Journal code: FML. ISSN: 0378-1097.

Netherlands PUB. COUNTRY:

JOURNAL ARTICLE) (JOURNAL ARTICLE)

English : ADAUDNAL

GENBANK-U12861 LIFE SECMENT: Priority Journals

ENTRY MONTH: 90966T OTHER SOURCE:

: AOHTUA

An Escherichia coli clone containing recombinant plasmid Cl9 was **AA** 

identified from a Treponema pallidum genomic DNA library by in situ

protein doublet of 39.2 and 38.2 kDa, designated immunoassay. E. coli maxicells containing pCl9 synthesized a treponemal

amino acids with a calculated molecular mass of 37.9 kpa The tpn38(b) gene is 1029 nucleotides long and encodes a protein of 343 fragment of pCl9 containing the tpn38(b) gene was subcloned and sequenced. is synthesized with a cleavable amino-terminal signal peptide. A 2.0-kb TpN38(b). Pulse-chase and protein processing studies showed that TpN38(b)

pallidum TpN35 lipoprotein and the Borrelia burgdorferi BmpA, BmpB, BmpC, . The deduced amino acid sequence of TpN38(b) has homology with the T.

and BmpD proteins.

DOCOMENT NUMBER: **₱L**622896 ACCESSION NUMBER: WEDFINE 7623296° rej wanke is of 25 medrine DUPLICATE 11

in treated patients with culture-confirmed erythema Evolution of the serologic response to Borrelia burgdorferi TITLE:

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Ydnero-Boseulejq W E: Nowskowski 1: Biffker 3: Coober D:

Nadelman R B; Wormser G P

Department of Pathology, New York Medical College, CORPORATE SOURCE:

.ASU ,alladlaV

N20-CCN SI0S80-01 (NIFWS) CONTRACT NUMBER:

(2MAIN) 80214AA-10A

ROI-AR43135

JOURNAL OF CLINICAL MICROBIOLOGY, (1996 Jan) 34 (1) 1-9. SOURCE:

Journal code: HSH. ISSN: 0095-1137.

United States PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE)

: ADAUDNAL English

Priority Journals LIFE SECWENT:

We investigated the appearance and evolution of immunoglobulin M (IgM) and 199612 ENTRY MONTH:

examination, only 22% were positive by the 1gG IB criteria of the Centers patients developed IgG antibodies as determined at a follow-up (OspC), 41 kDa, and 37 kDa. Although 89% of the The most frequent 19M bands at the baseline and the peak were of 24 kDa were seen at this time in patients with localized or disseminated disease. had a positive ELISA result and/or IgM IB result. Peak IgM antibody levels prior to treatment. At days 8 to 14 after the baseline, 91% of patients correlated directly with disease duration and/or evidence of dissemination Positive serology at the baseline and the rate of seroconversion Public Health Laboratory Directors for the interpretation of IB results. ior Disease Control and Prevention-Association of State and Territorial patients had a positive IgM IB result by using the criteria of the Centers baseline, 33% of the patients had a positive ELISA result and 43% of the immunosorbent assay and separate IgM and IgG immunoblots (IBs). At the collected serum samples were tested by commercial IgG-IgM enzyme-linked were prospectively evaluated for up to 1 year. A total of 257 serially erythema migrans (EM). All patients received antimicrobial treatment and IgG antibodies to Borrelia burgdorferi in 46 patients with culture-proven

Searched by Barb O'Bryen, STIC 308-4740

directly related to disease duration and/or dissemination prior to Public Health Laboratory Directors. The persistence of antibodies was for Disease Control and Prevention-Association of State and Territorial

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burgdorferi in individuals living in areas where Lyme disease is endemic. presence may be of assistance in confirming a recent infection with B. were most often seen in sera obtained within 1 month postbaseline. Their detectable for long periods, 38% of IgM mere still positive at 1 year postbaseline. IgM to antigens of 39, 58, 60, 66, or 93 kDa, conversely, treatment. Since IgM antibodies to the 24- and 41-kDa antigens remained

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Searched by Barb O'Bryen, STIC 308-4740
      single 235-55 rRNA gene unit. Representative isolate HT31T (T = type
                      contained a smaller 38-kDa endoflagellar protein and
        found that a small number of isolates obtained from I. persulcatus
 their genetic, biological, and immunological characteristics. However, we
  ticks have been classified as Borrelia burgdorferi sensu lato because of
   disease in Japan. Most spirochete isolates obtained from I. persulcatus
   The ixodid tick Ixodes persulcatus is the most important vector of Lyme
                                                                   ENTRY MONTH:
                                                     109661
                             CEMBANK-M60970; GEMBANK-M64312
            GENBANK-M64311; GENBANK-M75149; GENBANK-M60968;
            GENBYNK-I40297; GENBANK-M59293; GENBANK-M64309;
            GENBANK-D42192; GENBANK-L40596; GENBANK-L40597;
                                                                  OTHER SOURCE:
                                                                  LIFE SECMENT:
                                          Priority Journals
                                                    English
                                                                       : EAMGUAGE:
                        Journal; Article; (JOURNAL ARTICLE)
                                              United States
                                                                   FUB. COUNTRY:
                        Journal code: AWO. ISSN: 0020-7713.
                                        .01-P08 (4) 804-10.
    INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, (1995
                                                                         SOURCE:
                                             (GIAIN) 62848IA
                                                               CONTRACT NUMBER:
                             University, Hiroshima, Japan..
  Faculty of Pharmacy and Pharmaceutical Sciences, Fukuyama
                                                              CORPORATE SOURCE:
                                      McClelland M; Nakao M
 Fukunaga M; Takahashi Y; Tsuruta Y; Matsushita O; Ralph D;
                                                                         : AOHTUA
                          vector for Lyme disease in Japan.
nov., isolated from the ixodid tick Ixodes persulcatus, the
  Genetic and phenotypic analysis of Borrelia miyamotoi sp.
                                                                          TITLE:
                                                   LEL9T096
                                                               DOCUMENT NUMBER:
                                                              ACCESSION NUMBER:
                                       WEDFINE
                                                   LEL9T096
                                                  Tel Furmer 50 of 52 medrine
           DUPLICATE 13
                               (dd9L)
                                      Lyme disease and effective vaccines.
  infective Bb strains and can provide selective and sensitive assays for
 polypeptide is found only in highly infective Bb strains and not in low
                                    presence of Lyme disease. The 38 kDa
   the polypeptide in the blood of subjects can be used for detecting the
for detection. In particular, detection of the presence of antibodies to
   Tor the production of vaccines and in the production of antibodies and
specifically, Bb is strain Sh2 (5A3, 5A4 or 5A5. The polypeptide is used
(particularly 30 kDa) and nucleic acids encoding the polypeptides. More
      Borrelia burgdoferi (Bb). Also disclosed are other Bb polypeptides
    2-dimensional gel electrophoresis and which is produced in infectious
 A polypeptide is claimed which has a mol.wt. of 38,000 as determined by
                                                                              ΆA
                                          MbI: 62-136284 [18]
                                                                   OTHER SOURCE:
                                                       English
                                                                       : ADAUDNAL
                                                                 DOCOMENT TYPE:
                                                       Patent
                                                                 PRIORITY INFO:
                                     5661 qes 12 177421-56 2U
                                    APPLICATION INFO: WO 94-US10729 21 Sep 1994
                                       WO 9508568 30 Mar 1995
                                                                    PATENT INFO:
                                              .jey2-ssx9T.vinU
                                                               PATENT ASSIGNEE:
                                      Norris S J; Barbour A G
                                                                         : AOHTUA
                  detection of Lyme disease and in vaccine
         associated with highly infective strains used for
                         New Borrelia burgdoferi polypeptide;
                                                                          TITLE:
                                          ACCESSION NUMBER: 95-06970 BIOTECHDS
        FUSAMER 19 OF 25 BIOTECHDS COPYRIGHT 1999 DERWENT INFORMATION LTD
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HT31 is the type strain. propose the name Borrelia miyamotoi sp. nov. for this spirochete; strain isolates should be classified as members of a new Borrelia species. We Thus, the spirochetes isolated from I. persulcatus and closely related previously described Lyme disease borreliae and relapsing fever borreliae. The results showed that isolate HT31T is only distantly related to both matrix analyses were performed, and a phylogenetic tree was constructed. aligned with the 165 rRNA sequences of other Borrelia species. Distance sequence (length, 1,368 nucleotides) of strain HT31T was determined and of DNA relatedness with strain HT31T. In addition, the 16S rRNA gene Mone of the previously described species examined exhibited a high level burgdorferi, Borrelia garinii, and Borrelia afzelii) were only 8 to 13%. reassociation with the previously described Lyme disease borreliae (B. Borrelia parkeri, and Borrelia coriaceae. However, the levels of DNA levels of DNA relatedness (24 to 51%) with Borrelia hermsii, B. turicatae, hybridization experiments revealed that strain HT31T exhibited moderate DNA base composition of strain HT31T was 28.6 mol% G+C. DNA-DNA strain) had the same 23S rRNA gene physical map as Borrelia turicatae. The

DUPLICATE 14

DOCUMENT NUMBER: ACCESSION NUMBER: WEDFINE LSP9STP6 Tel PARMER SI OF 25 MEDLINE

Epitopes shared by unrelated antigens of Borrelia LST9STT6

burgdorferi.

Yuda P; Backenson P B; Coleman J L; Benach J L

Sanitarias, Instituto de Salud Carlos III, Madrid, Spain. Centro Nacional de Microbiologia, Virologia e Inmunologia

Journal code: GO7. ISSN: 0019-9567. INFECTION AND IMMUNITY, (1994 Mar) 62 (3) 1070-8.

United States

Journal; Article; (JOURNAL ARTICLE)

English

90166T ENTRY MONTH: Priority Journals; Cancer Journals LITE SECWENT: : **TANGUAGE**:

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PUB. COUNTRY:

CORPORATE SOURCE:

**POORCE:** 

: AOHTUA

TITLE:

reported for this antigen. The lowest reactive antigen had an M(r) of (p93) and had an NHZ-terminal sequence identical to the one previously strains. The reactive antigen with the highest  $M(\mathbf{r})$  was measured at 93 kDa whole-cell lysate of several American and European Borrelia burgdorferi in a Western blot (immunoblot) with approximately 30 polypeptides from a An immunoglobulin M kappa-chain murine monoclonal antibody (CAB) reacted

identity with glyceraldehyde-3-phosphate dehydrogenase of other bacteria molecular mass of approximately 38.5 kDa had a strong procked to Edman degradation. Finally, one sequenced polypeptide with a burgdorferi. Two other antigens at approximately 49 and 47 kDa were approximately 72-kDa polypeptide to be identical to the Dnak homolog of B. Amino-terminal sequences of other reactive polypeptides showed one internal and thus less likely to be degraded by experimental procedures. insoluble fraction of a Triton X-114 partition indicated that they were treatment of intact organisms and recovery of the antigens in the likely not due to the action of endogenous proteases. Likewise, protease reactivity, indicating that if such degradation existed, it was most burgdorferi with protease inhibitors did not result in changes in CAB could recognize shared epitopes in different antigens. Treatment of B. degradation of p93 has already been reported, and to determine whether CAB degradation of the antigen with the highest M(r), since such spontaneous study was to determine whether the broad reactivity of CAB could be due to narrow acidic range, between 5.4 and 6.2. Thus, the objective of this 16,000. All antigens recognized by CAB had isoelectric points within a

Searched by Barb O'Bryen, STIC 308-4740

acid residues 357 to 371 of p93 was identified. Evidence is presented for five, unrelated antigens of B. burgdorferi. A linear epitope within amino indicate the presence of a shared epitope in at least three, possibly reactivity may be due to fragmentation of p93, there is strong evidence to and vertebrates. Thus, while it cannot be ruled out that some of the CAB

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INFECTION, (1994 Nov-Dec) 22 (6) 401-6. **Милсћел, Germany..** Dermatologische Klinik, Ludwig-Maximilians-Universitat, CORPORATE SOURCE: Schaller M; Neubert U : AOHTUA penzylpenicillin. Ultrastructure of Borrelia burgdorferi after exposure to TITLE: DOCUMENT NUMBER: 95213112 **YCCEZZION NOMBEK:** WEDLINE 95213112 Tel Furmer SS of SS Medrine DUPLICATE 15 various antigens. indicate possible genetic and/or functional relatedness among these conserved amino acid sequences necessary for these shared epitopes homolog, which bears strong amino acid identity with the p93 epitope. The a discontinuous epitope in the carboxy-terminal region of the DnaK

ENTRY MONTH: L0966T Priority Journals LIFE SECWENT: English : EDAGUAGE: Journal; Article; (JOURNAL ARTICLE)

GERMANY: Germany, Federal Republic of

Journal code: GO8. ISSN: 0300-8126.

The aim of this study was to investigate the morphological changes of ЯA

presence of "spheroplasts" at the same concentration. (iv) Structural sheath at a penicillin concentration of 0.125 mg/l. (iii) The waveform of the borrelial cells and complete loss of the outer penicillin concentration of 0.0625 mg/l. (ii) A characteristic irregular discovered: (i) Numerous outer sheath blebs at a opserved by electron microscopy. The following alterations were cysrscferistic ultrastructural changes when exposed to penicillin, were morphological structures of untreated spirochetes, as well as their (MIC) was determined to be 0.5 mg/l by broth dilution method. The penicillin G for 5 days. The in vitro minimal inhibitory concentration medium and exposed to increasing concentrations  $(0.0625 \text{ mg/L}^{-2} \text{ mg/L})$  of B. burgdorferi from an erythema migrans lesion was cultivated in BSK II Borrelia burgdorferi associated with penicillin treatment. An isolate of

protoplasmic cylinder complex into several parts at penicillin pattern at a penicillin concentration of 0.125 mg/l. (v) Disruption of the changes of the protoplasmic cylinder complex which showed an irregular

penicillin concentrations of 1 mg/l and 2 mg/l. concentrations of 0.25 mg/l and 0.5 mg/l. (vi) Severe cytolysis at

Bacterial expression vectors containing DNA encoding TITLE: DOCUMENT NUMBER: T18:249317 1993:249317 CAPLUS ACCESSION NUMBER:

Stover, Charles K. INAENTOR(S): preparation of vaccines secretion signals of lipoproteins and their uses for

Medimmune, Inc., USA PATENT ASSIGNEE(S):

Tel Answer 23 of 25 Caplus Copyright 1999 Acs

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CODEN: BIXXDS PCT Int. Appl., 115 pp. **SONKCE:** 

Patent DOCUMENT TYPE:

FAMILY ACC. NUM. COUNT: 7 English **TANGUAGE:** 

PATENT INFORMATION:

FUB. COUNTRY:

SOURCE:

STZI83 UA

19921021 0116S-See1 UA 19930521 ſΑ 0116SS6 UA BM: FI' BE' CH' DE' DK' ES' EB' GB' E' IL' IN' WC' NI' SE W: AU, CA, JP 19921021 S7062U-2661 OW 19930429 ſΑ 76870E9 OW DATE APPLICATION NO. KIND DYTE PATENT NO.

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55-70. 32 ref.
 Veterinary Microbiology, (1992) Vol. 31, No. 1, pp.
                                                                         SOURCE:
                                         ZMI, Canada.
 Immunology, University of Guelph, Guelph, Ont. NiG
           Department of Veterinary Microbiology and
                                                              CORPORATE SOURCE:
                        Mendoza, L.; Prescott, J. F.
                                                                         AUTHOR:
    axial filament enzyme-linked immunosorbent assay
     Serodiagnosis of leptospirosis in pigs using an
                                                                           TITLE:
                                                                DOCUMENT NUMBER:
                                            922268208
                                      92:70811 CABA
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                                  Tel Answer 25 of 25 Caba Copyright 1999 Cabi
                    staining of lesion exudate or formalin-fixed tissue.
           (38 ref)
  with fluorescein isothiocyanate and used to diagnose syphilis by direct
                           pomona, or with normal rabbit testicle tissue.
    The mAbs were labeled
                    Borrelia burgdorferi and Leptospira interrogans serovar
              Treponema refringens Noguchi, or other spirochetes, such as
     not react with Treponema phagedenis Reiter, Treponema denticola MRB,
subsp. pallidum Nichols and T. pallidum subsp. pertenue Gauthier, but did
                        DAL-1, and with the 37 kDa antigen of T. pallidum
                     LLO/2 and LLP/73 reacted with the 37 kDa molecule of
     were cloned twice by limiting dilution. Monoclonal antibodies (MAbs)
   microimmunofluorescent antibody and ELISA procedure. Selected cultures
            Hybrids were selected in HAT medium and assayed by a
 bysemacytoma cells by mixing in 4:1 ratio in the presence of PEG 1500 at
           a final booster on day 70. Spleen cells were fused with SP2/0
 injections in incomplete adjuvant were given on days 15, 29 and 66, with
                 phosphate-buffered saline-Freund's incomplete adjuvant.
          3 More
        pallidum subsp. pallidum street strain DAL-1 by i.p. injection in
  BALB/c mice (4-5-wk-old) were immunized with Percoll-purified Treponema
                                                                              ЯA
                                                       English
                                                                       TANGUAGE:
                                                       lournal
                                                                  DOCUMENT TYPE:
                                                 CODEN: 1CWIDM
                Disease Control, Atlanta, Georgia 30333, USA. J.Clin.Microbiol.; (1992) 30, 4, 831-38
                                                                          SOURCE:
       Research, Centers for Infectious Diseases, Centers for
         Division of Sexually Transmitted Diseases Laboratory
                                                                       :NOITADO1
           Ito E; Hunter E E; George R W; Pope V; *Larsen S A
                                                                         : AOHTUA
                                                  diagnosis
 Treponema pallidum subsp. pallidum detection for syphilis
                                   with a monoclonal antibody;
 Specific immunofluorescent staining of pathogenic treponemes
                                                                           TITLE:
                                           YCCESSION NOWBEE: 65-02816 BIOLECHDS
        FUSMER 24 OF 25 BIOTECHDS COPYRIGHT 1999 DERWENT INFORMATION LTD
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                                  transformed with plasmids was also shown.
 and the OspA antigen was demonstrated. Immunization of mice with the BCG
   bromorer, the signal sequence of the 19-kDa antigen of M. tuberculosis,
     Construction of plasmids, e.g. p2619::OspA, contg. the BCG HSP60 gene
                    burgdorferi and used in vaccines against Lyme disease.
                      encoding an Outer Surface Protein A or B of Borrelia
        Mycobacterium such as BCG may be transformed with a plasmid vector
         the lipoprotein and the antigen protein can be used in a vaccine.
   Transformed bacteria expressing a chimeric gene for a fusion protein of
     the presentation of the protein on the surface of the bacterial host.
 expression vector increases the immunogenicity of the protein by enabling
            of a lipoprotein and a heterologous protein antigen is prepd.
  A bacterial expression vector conty, a DNA encoding the secretion signal
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of 35 kDa and 34.5 kDa. Immunoblot analysis using antiserum to the AF immunoblotting. Analysis by SDS-PAGE of the purified preparation showed sulphate polyacrylamide gel electrophoresis (SDS-PAGE), and The axial filament (AF) from Leptospira interrogans serovar canicola was English

the use of AF in immunodiagnosis of leptospirosis in other species. antigen source. It is suggested that these findings may be extrapolated to sonicated whole cells can substitute excellently for purified AF as the antigen for the serological diagnosis of leptospirosis in swine and that coucjnded that the AF-ELISA can be used effectively as a species-specific correlation was observed between AF-ELISA and WC-ELISA (r=0.97). It was cells (WC) of serovar canicola were used in an ELISA (WC-ELISA), high between titres detected in the AF-ELISA and the MAT. When sonicated whole in comparison to the MAT (r = 0.4). Only moderate correlation was observed serovars. A sensitivity of 97.1% and specificity of 93.1% was determined the microscopic agglutination test (MAT) against one or more leptospiral tested in an AF-ELISA against sera from 260 pigs, many of which reacted in burgdorferi but only a very minor reaction with leptospiral AF. The AF was hyodysenteriae showed a marked reaction with a 41 kDa band of B. not detect the leptospiral AF antigen. Immunoblots with antiserum to T. slightly in comparison to leptospiral AF. Antibody of B. burgdorferi did burgdorferi moderately and of Treponema hyodysenteriae only bratislava detected the 35 and 34.5 kDa AF bands to Borrelia at 33 and 32 kDa. Immunoblots with antiserum to whole cells of serovar Antisera prepared against leptospiral serovars also identified minor bands minor bands of molecular weight 43, 39 and 37 kDa. reaction against the 41, 35 and 34.5 kDa protein bands, as well as against against sonicated leptospires of a variety of serovars showed prominent relatively weak bands of molecular size 42 kDa and 21 kDa and strong bands microscopic examination, by protein-A immunogold labelling, sodium dodecyl sarcosyl treated whole cells. Isolation of AF was confirmed by electron isolated by caesium chloride density gradient centrifugation of 2%

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